

PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 478

ID ACD85415 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 479

ID ACD86029 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 480

ID ACF76025 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 481

ID ACF60925 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 482

ID ACH05812 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 483

ID ADA82956 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 484

ID ACF56071 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003068680-A1.

PD 10-APR-2003.

Query Match 6.2%; Score 143.2; DB 9; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 485

ID ACF55457 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068762-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 486

ID ADB86264 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003054472-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 487

ID ACF56378 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068708-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 488

ID ACF56685 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068713-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 489

ID ACF55764 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068761-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 490

ID ACF55150 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003068771-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 491

ID ADD05994 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003087376-A1.

PD 08-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 492
 ID ADG02989 standard; cDNA; 2974 BP.
 DE Novel human secreted and transmembrane protein PRO6239 cDNA.
 PN US2003207397-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 10; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 493
 ID ADG01696 standard; cDNA; 2974 BP.
 DE Novel human secreted and transmembrane protein PRO6239 cDNA.
 PN US2003207399-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 10; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 494
 ID ADF95871 standard; cDNA; 2974 BP.
 DE Novel human secreted and transmembrane protein PRO6239 cDNA.
 PN US2003207398-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 10; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 495
 ID ADG12686 standard; cDNA; 2974 BP.
 DE Novel human secreted and transmembrane protein PRO6239 cDNA.
 PN US2003207392-A1.
 PD 06-NOV-2003.
 Query Match 6.2%; Score 143.2; DB 10; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 496
 ID ADH09346 standard; cDNA; 2974 BP.
 DE Human PRO polynucleotide #261.
 PN US2003207395-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 10; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 497
 ID ABX78788 standard; cDNA; 2974 BP.
 DE Human PRO polynucleotide #261.
 PN US2003027272-A1.
 PD 06-FEB-2003..
 Query Match 6.2%; Score 143.2; DB 10; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 498
 ID ACA75760 standard; cDNA; 2974 BP.
 DE Novel human secreted and transmembrane protein PRO6239 cDNA.
 PN US2003032127-A1.
 PD 13-FEB-2003.
 Query Match 6.2%; Score 143.2; DB 10; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 499
 ID ACA71240 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 500
ID ACC87768 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 501
ID ACC87154 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 502
ID ACD04327 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 503
ID ACA69658 standard; cDNA; 2974 BP.
DE cDNA encoding human PRO polypeptide #261.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 504
ID ACA90503 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 505
ID ACC89610 standard; cDNA; 2974 BP.
DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 506
ID ACA98401 standard; cDNA; 2974 BP.
DE Novel human secreted and transmembrane protein PRO6239 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;
RESULT 507
ID ACA94043 standard; cDNA; 2974 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003036149-A1.

PD 20-FEB-2003.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 508

ID ACD15436 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003044923-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 509

ID ACD09023 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003040062-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 510

ID ACC96943 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003040056-A1.

PD 27-FEB-2003.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 511

ID ACF15664 standard; cDNA; 2974 BP.

DE Human secreted polypeptide PRO6239-encoding cDNA, SEQ ID NO:521.

PN US2003044926-A1.

PD 06-MAR-2003.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 512

ID ACA73031 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003036140-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 513

ID ACD03203 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003013153-A1.

PD 16-JAN-2003.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 514

ID ACD02018 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003017544-A1.

PD 23-JAN-2003.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 515

ID ACA92210 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003027277-A1.

PD 06-FEB-2003.

Query Match 6.2%; Score 143.2; DB 10; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 516

ID ADL33125 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003207396-A1.

PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 11; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 517

ID ADM30661 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003073813-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 11; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 518

ID ADE74658 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003211572-A1.

PD 13-NOV-2003.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 519

ID ADE75270 standard; cDNA; 2974 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #261.

PN US2003211574-A1.

PD 13-NOV-2003.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 520

ID ADF96483 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003215909-A1.

PD 20-NOV-2003.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 521

ID ADG04754 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003215912-A1.

PD 20-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 522

ID ADG00914 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003215911-A1.

PD 20-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;
Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 523

ID ADG83170 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003215910-A1.

PD 20-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 524

ID ADH26451 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2003068770-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 525

ID ADH33420 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2003068768-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 526

ID ADJ55159 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2004023321-A1.

PD 05-FEB-2004.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 527

ID ADL06423 standard; cDNA; 2974 BP.

DE Human tumour-associated antigenic target (TAT) cDNA sequence #3.

PN WO2004016225-A2.

PD 26-FEB-2004.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 528

ID ADJ64930 standard; cDNA; 2974 BP.

DE Human PRO polynucleotide #261.

PN US2004038337-A1.

PD 26-FEB-2004.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 529

ID ADM31826 standard; cDNA; 2974 BP.

DE Novel human secreted and transmembrane protein PRO6239 cDNA.

PN US2004048334-A1.

PD 11-MAR-2004.

PA (GETH) GENENTECH INC.

Query Match 6.2%; Score 143.2; DB 12; Length 2974;

Best Local Similarity 48.3%; Pred. No. 5.7e-31;

RESULT 530

ID ADM36873 standard; cDNA; 2974 BP.
 DE Novel human secreted and transmembrane protein PRO6239 cDNA.
 PN US2004053358-A1.
 PD 18-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 12; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 531
 ID ADM40678 standard; cDNA; 2974 BP.
 DE Novel human secreted and transmembrane protein PRO6239 cDNA.
 PN US2004048335-A1.
 PD 11-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 12; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 532
 ID ADN38286 standard; cDNA; 2974 BP.
 DE Novel human secreted and transmembrane protein PRO6239 cDNA.
 PN US2004091959-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 6.2%; Score 143.2; DB 12; Length 2974;
 Best Local Similarity 48.3%; Pred. No. 5.7e-31;
 RESULT 533
 ID ADP72670 standard; DNA; 1858 BP.
 DE Renal toxin progression gene marker #1259.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 6.1%; Score 142; DB 12; Length 1858;
 Best Local Similarity 51.3%; Pred. No. 9.6e-31;
 RESULT 534
 ID ABN75524 standard; cDNA; 336 BP.
 DE Human ORF471 cDNA, SEQ ID NO:941.
 PN WO200190366-A2.
 PD 29-NOV-2001.
 PA (CURA-) CURAGEN CORP.
 Query Match 6.1%; Score 141.8; DB 6; Length 336;
 Best Local Similarity 65.9%; Pred. No. 3.5e-31;
 RESULT 535
 ID ADB53826 standard; DNA; 1947 BP.
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4368.
 PN WO2003065993-A2.
 PD 14-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 6.1%; Score 141.8; DB 10; Length 1947;
 Best Local Similarity 48.1%; Pred. No. 1.1e-30;
 RESULT 536
 ID ABT42419 standard; DNA; 1947 BP.
 DE Toxicity modelling related rat gene SEQ ID No 2121.
 PN WO200295000-A2.
 PD 28-NOV-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 6.1%; Score 141.8; DB 10; Length 1947;
 Best Local Similarity 48.1%; Pred. No. 1.1e-30;
 RESULT 537
 ID ADP72852 standard; DNA; 1947 BP.

DE Renal toxin progression gene marker #1441.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.

Query Match 6.1%; Score 141.8; DB 12; Length 1947;
Best Local Similarity 48.1%; Pred. No. 1.1e-30;

RESULT 538

ID ABX72195 standard; cDNA; 1705 BP.
DE Human NOVX polynucleotide #26.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.

Query Match 6.1%; Score 141.6; DB 8; Length 1705;
Best Local Similarity 48.2%; Pred. No. 1.2e-30;

RESULT 539

ID AAD59158 standard; cDNA; 1620 BP.
DE Human UDP-glucuronosyltransferase cDNA #2.
PN US2003073105-A1.
PD 17-APR-2003.
PA (LASE/) LASEK A K W.
PA (SORN/) SORNASSE T.

Query Match 6.1%; Score 141.2; DB 10; Length 1620;
Best Local Similarity 48.8%; Pred. No. 1.5e-30;

RESULT 540

ID ABX72194 standard; cDNA; 3050 BP.
DE Human NOVX polynucleotide #25.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.

Query Match 6.1%; Score 141; DB 8; Length 3050;
Best Local Similarity 48.2%; Pred. No. 2.6e-30;

RESULT 541

ID ADB58614 standard; DNA; 1593 BP.
DE Toxicity-related gene, SEQ ID 3640.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.

Query Match 6.0%; Score 140; DB 10; Length 1593;
Best Local Similarity 51.2%; Pred. No. 3.4e-30;

RESULT 542

ID ADB53262 standard; DNA; 1593 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3804.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.

Query Match 6.0%; Score 140; DB 10; Length 1593;
Best Local Similarity 51.2%; Pred. No. 3.4e-30;

RESULT 543

ID ABT42206 standard; DNA; 1593 BP.
DE Toxicity modelling related rat gene SEQ ID No 1908.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.

Query Match 6.0%; Score 140; DB 10; Length 1593;
Best Local Similarity 51.2%; Pred. No. 3.4e-30;

RESULT 544

ID AAL41490 standard; DNA; 1639 BP.

DE Drug metabolising enzyme encoding DNA - 7493833CB1.
 PN WO200266654-A2..
 PD 29-AUG-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 6.0%; Score 139.8; DB 6; Length 1639;
 Best Local Similarity 49.2%; Pred. No. 4e-30;
 RESULT 545
 ID ADA11075 standard; cDNA; 1714 BP.
 DE Human cDNA differentially expressed in colon cancer #138.
 PN US2002160382-A1.
 PD 31-OCT-2002.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 6.0%; Score 139.2; DB 9; Length 1714;
 Best Local Similarity 49.8%; Pred. No. 6.2e-30;
 RESULT 546
 ID ABL68501 standard; DNA; 1855 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:6838.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 6.0%; Score 139.2; DB 6; Length 1855;
 Best Local Similarity 49.8%; Pred. No. 6.6e-30;
 RESULT 547
 ID ABL68868 standard; DNA; 1855 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:7205.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 6.0%; Score 139.2; DB 6; Length 1855;
 Best Local Similarity 49.8%; Pred. No. 6.6e-30;
 RESULT 548
 ID ABN95622 standard; DNA; 1855 BP.
 DE Gene #2120 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 6.0%; Score 139.2; DB 6; Length 1855;
 Best Local Similarity 49.8%; Pred. No. 6.6e-30;
 RESULT 549
 ID ADD71099 standard; DNA; 1855 BP.
 DE Human UDP glycosyltransferase 2 family B7 gene SEQ ID NO:103.
 PN WO2003061564-A2.
 PD 31-JUL-2003.
 PA (GENE-) GENE LOGIC INC.
 PA (LGBI-) LG BIOMEDICAL INST.
 Query Match 6.0%; Score 139.2; DB 10; Length 1855;
 Best Local Similarity 49.8%; Pred. No. 6.6e-30;
 RESULT 550
 ID ADR46644 standard; DNA; 1855 BP.
 DE Cancer-associated protein coding sequence, SEQ ID 57.
 PN WO2004073657-A2.
 PD 02-SEP-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 6.0%; Score 139.2; DB 13; Length 1855;
 Best Local Similarity 49.8%; Pred. No. 6.6e-30;
 RESULT 551

ID AAD45991 standard; cDNA; 1991 BP.
 DE Human UGT2B7 cDNA.
 PN WO200259375-A2.
 PD 01-AUG-2002.
 PA (UYCH-) UNIV CHICAGO.
 Query Match 6.0%; Score 139.2; DB 6; Length 1991;
 Best Local Similarity 49.8%; Pred. No. 6.9e-30;
 RESULT 552
 ID ADP72910 standard; DNA; 1846 BP.
 DE Renal toxin progression gene marker #1499.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.9%; Score 136.8; DB 12; Length 1846;
 Best Local Similarity 50.9%; Pred. No. 3.4e-29;
 RESULT 553
 ID ADP72818 standard; DNA; 1844 BP.
 DE Renal toxin progression gene marker #1407.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.9%; Score 136.4; DB 12; Length 1844;
 Best Local Similarity 48.6%; Pred. No. 4.5e-29;
 RESULT 554
 ID AAV15900 standard; cDNA; 2107 BP.
 DE Uridine diphospho-glucuronosyltransferase 2B17 (UGT2B17) encoding cDNA.
 PN WO9744466-A1.
 PD 27-NOV-1997.
 PA (ENDO-) ENDORECHERCHE INC.
 Query Match 5.9%; Score 136.4; DB 2; Length 2107;
 Best Local Similarity 49.5%; Pred. No. 4.9e-29;
 RESULT 555
 ID ADR07753 standard; cDNA; 2172 BP.
 DE Full length human cDNA useful for treating neurological disease Seq 1259.
 PN EP1447413-A2.
 PD 18-AUG-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 5.9%; Score 136.4; DB 13; Length 2172;
 Best Local Similarity 48.0%; Pred. No. 5e-29;
 RESULT 556
 ID AAS78773 standard; cDNA; 2448 BP.
 DE DNA encoding novel human diagnostic protein #14577.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 136.4; DB 5; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
 RESULT 557
 ID AAS78611 standard; cDNA; 2448 BP.
 DE DNA encoding novel human diagnostic protein #14415.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 136.4; DB 5; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
 RESULT 558
 ID AAS84057 standard; cDNA; 2448 BP.

DE DNA encoding novel human diagnostic protein #19861.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 136.4; DB 5; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
 RESULT 559
 ID AAS74393 standard; cDNA; 2448 BP.
 DE DNA encoding novel human diagnostic protein #10197.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 136.4; DB 5; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
 RESULT 560
 ID AAS72022 standard; cDNA; 2448 BP.
 DE DNA encoding novel human diagnostic protein #7826.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.9%; Score 136.4; DB 5; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
 RESULT 561
 ID ABL67995 standard; DNA; 2448 BP.
 DE Ovary cancer related gene sequence SEQ ID NO:6332.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 5.9%; Score 136.4; DB 6; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
 RESULT 562
 ID ACA89932 standard; cDNA; 2448 BP.
 DE Gene differentially regulated in cardiovascular disease #53.
 PN WO2003031650-A2.
 PD 17-APR-2003.
 PA (FARB) BAYER AG.
 Query Match 5.9%; Score 136.4; DB 8; Length 2448;
 Best Local Similarity 48.0%; Pred. No. 5.4e-29;
 RESULT 563
 ID AAZ95200 standard; DNA; 1854 BP.
 DE Human UDP-glucuronosyltransferase 2B7 nucleotide sequence.
 PN WO200006776-A1.
 PD 10-FEB-2000.
 PA (AXYS-) AXYS PHARM INC.
 Query Match 5.9%; Score 136; DB 3; Length 1854;
 Best Local Similarity 49.6%; Pred. No. 5.9e-29;
 RESULT 564
 ID ADC39064 standard; cDNA; 3005 BP.
 DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 3.
 PN WO2003010327-A2.
 PD 06-FEB-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.8%; Score 135.4; DB 10; Length 3005;
 Best Local Similarity 48.4%; Pred. No. 1.2e-28;
 RESULT 565
 ID AAC65396 standard; cDNA; 1650 BP.
 DE Human carbohydrate-modifying enzyme cDNA Incyte ID No: 2912330CB1.

PN WO200063351-A2.
 PD 26-OCT-2000.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.8%; Score 133.8; DB 3; Length 1650;
 Best Local Similarity 49.3%; Pred. No. 2.5e-28;
 RESULT 566
 ID ADR25043 standard; DNA; 1894 BP.
 DE Breast cancer prognosis marker #904.
 PN WO2004065545-A2.
 PD 05-AUG-2004.
 PA (ROSE-) ROSETTA INPHARMATICS LLC.
 PA (NECA-) NETHERLANDS CANCER INST.
 Query Match 5.8%; Score 133.8; DB 13; Length 1894;
 Best Local Similarity 49.1%; Pred. No. 2.7e-28;
 RESULT 567
 ID ADG47988 standard; DNA; 1756 BP.
 DE Human UDP-glucuronosyl transferase (UGT) gene.
 PN US2003101002-A1.
 PD 29-MAY-2003.
 PA (BART/) BARTHA G T.
 PA (WALK/) WALKER M.
 Query Match 5.8%; Score 133.4; DB 12; Length 1756;
 Best Local Similarity 48.7%; Pred. No. 3.4e-28;
 RESULT 568
 ID AAS91380 standard; cDNA; 1766 BP.
 DE DNA encoding novel human diagnostic protein #27184.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.8%; Score 133.4; DB 5; Length 1766;
 Best Local Similarity 48.7%; Pred. No. 3.4e-28;
 RESULT 569
 ID ADE53677 standard; cDNA; 1829 BP.
 DE Human prostate cancer cDNA #24.
 PN US2003190640-A1.
 PD 09-OCT-2003.
 PA (FARI/) FARIS M.
 PA (PEAR/) PEARSON C I.
 Query Match 5.7%; Score 133.2; DB 10; Length 1829;
 Best Local Similarity 49.3%; Pred. No. 4e-28;
 RESULT 570
 ID ADO42268 standard; cDNA; 1662 BP.
 DE Human NOVX polynucleotide #59.
 PN US2004058338-A1.
 PD 25-MAR-2004.
 PA (AGEE/) AGEE M L.
 PA (ALSO/) ALSOBROOK J P.
 PA (ANDE/) ANDERSON D W.
 PA (BERG/) BERGHS C.
 PA (BOLD/) BOLDOG F L.
 PA (BURG/) BURGESS C E.
 PA (CATT/) CATTERTON E.
 PA (DIPI/) DIPIPO V A.
 PA (EDIN/) EDINGER S R.
 PA (EISE/) EISEN A.
 PA (ELLE/) ELLERMAN K.
 PA (GANG/) GANGOLLI E A.

PA (GERL/) GERLACH V.
 PA (GORM/) GORMAN L.
 PA (ROTH/) ROTHBERG B G.
 PA (GUOX/) GUO X S.
 PA (HERR/) HERRMANN J L.
 PA (HALV/) HALVORSEN Y.
 PA (JIWW/) JI W.
 PA (KEKU/) KEKUDA R.
 PA (KHRA/) KHRAMTSOV N V.
 PA (LARO/) LAROCHELLE W J.
 PA (LEPL/) LEPLEY D M.
 PA (LILL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MILL/) MILLER C E.
 PA (ORTT/) ORT T.
 PA (PADI/) PADIGARU M.
 PA (PATT/) PATTURAJAN M.
 PA (PENA/) PENNA C E A.
 PA (PEYM/) PEYMAN J A.
 PA (RIEG/) RIEGER D K.
 PA (ROTH/) ROTHENBERG M E.
 PA (SHEN/) SHENOY S G.
 PA (SMIT/) SMITHSON G.
 PA (SPAD/) SPADERNA S K.
 PA (SPYT/) SPYTEK K A.
 PA (STON/) STONE D J.
 PA (TAUP/) TAUPIER R J.
 PA (VERN/) VERNET C A M.
 PA (VOSS/) VOSS E Z.
 PA (ZHON/) ZHONG M.

Query Match 5.7%; Score 133; DB 12; Length 1662;
 Best Local Similarity 47.7%; Pred. No. 4.3e-28;

RESULT 571

ID ADR19685 standard; DNA; 1614 BP.
 DE Human drug metabolising enzyme (DME)-6 gene sequence.
 PN WO200226988-A2.
 PD 04-APR-2002.
 PA (INCY-) INCYTE GENOMICS INC.

Query Match 5.7%; Score 132; DB 7; Length 1614;
 Best Local Similarity 48.4%; Pred. No. 8.4e-28;

RESULT 572

ID AAD57503 standard; cDNA; 1608 BP.
 DE Human enzyme (ENZM) cDNA #15.
 PN WO2003052075-A2.
 PD 26-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.

Query Match 5.7%; Score 131.6; DB 9; Length 1608;
 Best Local Similarity 49.2%; Pred. No. 1.1e-27;

RESULT 573

ID ADB58692 standard; DNA; 1846 BP.
 DE Toxicity-related gene, SEQ ID 3718.
 PN WO2003064624-A2.
 PD 07-AUG-2003.
 PA (GENE-) GENE LOGIC INC.

Query Match 5.7%; Score 131.6; DB 10; Length 1846;
 Best Local Similarity 48.4%; Pred. No. 1.2e-27;

RESULT 574

ID ADB53380 standard; DNA; 1846 BP.
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3922.
 PN WO2003065993-A2.
 PD 14-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.7%; Score 131.6; DB 10; Length 1846;
 Best Local Similarity 48.4%; Pred. No. 1.2e-27;
 RESULT 575
 ID ADP72819 standard; DNA; 1846 BP.
 DE Renal toxin progression gene marker #1408.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.7%; Score 131.6; DB 12; Length 1846;
 Best Local Similarity 48.4%; Pred. No. 1.2e-27;
 RESULT 576
 ID AAZ95199 standard; DNA; 2092 BP.
 DE Human UDP-glucuronosyltransferase 2B4 nucleotide sequence.
 PN WO200006776-A1.
 PD 10-FEB-2000.
 PA (AXYS-) AXYS PHARM INC.
 Query Match 5.7%; Score 131.6; DB 3; Length 2092;
 Best Local Similarity 49.2%; Pred. No. 1.3e-27;
 RESULT 577
 ID ABN96789 standard; DNA; 2123 BP.
 DE Gene #3287 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.6%; Score 130; DB 6; Length 2123;
 Best Local Similarity 49.1%; Pred. No. 4e-27;
 RESULT 578
 ID AAD06860 standard; DNA; 1722 BP.
 DE Human breast cancer specific gene-2 (BCSG-2) #2.
 PN WO200137779-A2.
 PD 31-MAY-2001.
 PA (DIAD-) DIADEXUS INC.
 Query Match 5.6%; Score 129; DB 5; Length 1722;
 Best Local Similarity 48.0%; Pred. No. 6.9e-27;
 RESULT 579
 ID ABN97261 standard; DNA; 2799 BP.
 DE Gene #3759 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.6%; Score 129; DB 6; Length 2799;
 Best Local Similarity 48.0%; Pred. No. 9.6e-27;
 RESULT 580
 ID ADD71006 standard; DNA; 2799 BP.
 DE Human UDP glycosyltransferase 2 family B10 gene SEQ ID NO:10.
 PN WO2003061564-A2.
 PD 31-JUL-2003.
 PA (GENE-) GENE LOGIC INC.
 PA (LGBI-) LG BIOMEDICAL INST.
 Query Match 5.6%; Score 129; DB 10; Length 2799;
 Best Local Similarity 48.0%; Pred. No. 9.6e-27;
 RESULT 581

ID ADO00385 standard; cDNA; 1593 BP.
DE Novel human cDNA sequence #1200.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.5%; Score 128.4; DB 12; Length 1593;
Best Local Similarity 49.0%; Pred. No. 1e-26;
RESULT 582
ID ADN98816 standard; cDNA; 1593 BP.
DE Novel human cDNA sequence #416.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.5%; Score 128.4; DB 12; Length 1593;
Best Local Similarity 49.0%; Pred. No. 1e-26;
RESULT 583
ID AAZ95206 standard; DNA; 1976 BP.
DE Human UDP-glucuronosyltransferase 2B15 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.
Query Match 5.5%; Score 128.4; DB 3; Length 1976;
Best Local Similarity 49.0%; Pred. No. 1.1e-26;
RESULT 584
ID ABK84210 standard; cDNA; 2090 BP.
DE Human cDNA differentially expressed in granulocytic cells #781.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.5%; Score 128.4; DB 6; Length 2090;
Best Local Similarity 49.0%; Pred. No. 1.2e-26;
RESULT 585
ID ABN96795 standard; DNA; 2090 BP.
DE Gene #3293 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 5.5%; Score 128.4; DB 6; Length 2090;
Best Local Similarity 49.0%; Pred. No. 1.2e-26;
RESULT 586
ID ABT17080 standard; DNA; 2090 BP.
DE Androgen-independent prostate cancer-related DNA - SEQ ID No 11.
PN WO200298358-A2.
PD 12-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.5%; Score 128.4; DB 8; Length 2090;
Best Local Similarity 49.0%; Pred. No. 1.2e-26;
RESULT 587
ID AAD43928 standard; cDNA; 1413 BP..
DE Human UDP-glycosyltransferase cDNA.
PN US6383789-B1.
PD 07-MAY-2002.
PA (PEKE) PE CORP NY.
Query Match 5.5%; Score 127.6; DB 6; Length 1413;
Best Local Similarity 50.1%; Pred. No. 1.6e-26;
RESULT 588
ID ADE48040 standard; cDNA; 1413 BP.

DE Human UDP-glycosyltransferase protein cDNA.
 PN US2002182692-A1.
 PD 05-DEC-2002.
 PA (PEKE) PE CORP NY.
 Query Match 5.5%; Score 127.6; DB 12; Length 1413;
 Best Local Similarity 50.1%; Pred. No. 1.6e-26;
 RESULT 589
 ID ADQ14303 standard; cDNA; 1413 BP.
 DE Human UDP-glycosyltransferase cDNA.
 PN US2004132089-A1.
 PD 08-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 5.5%; Score 127.6; DB 12; Length 1413;
 Best Local Similarity 50.1%; Pred. No. 1.6e-26;
 RESULT 590
 ID ADA10927 standard; cDNA; 2150 BP.
 DE Human cDNA differentially expressed in colon cancer #31.
 PN US2002160382-A1.
 PD 31-OCT-2002.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 5.5%; Score 127.2; DB 9; Length 2150;
 Best Local Similarity 49.6%; Pred. No. 2.8e-26;
 RESULT 591
 ID ADE53678 standard; cDNA; 2150 BP.
 DE Human prostate cancer cDNA #25.
 PN US2003190640-A1.
 PD 09-OCT-2003.
 PA (FARI/) FARIS M.
 PA (PEAR/) PEARSON C I.
 Query Match 5.5%; Score 127.2; DB 10; Length 2150;
 Best Local Similarity 49.6%; Pred. No. 2.8e-26;
 RESULT 592
 ID AAS69710 standard; cDNA; 1859 BP.
 DE DNA encoding novel human diagnostic protein #5514.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.4%; Score 126.4; DB 5; Length 1859;
 Best Local Similarity 48.8%; Pred. No. 4.4e-26;
 RESULT 593
 ID AAS69711 standard; cDNA; 2802 BP.
 DE DNA encoding novel human diagnostic protein #5515.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.4%; Score 125.4; DB 5; Length 2802;
 Best Local Similarity 47.7%; Pred. No. 1.1e-25;
 RESULT 594
 ID ABN97347 standard; DNA; 2093 BP.
 DE Gene #3845 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.4%; Score 125.2; DB 6; Length 2093;
 Best Local Similarity 48.7%; Pred. No. 1.1e-25;
 RESULT 595

ID ADH13736 standard; DNA; 1045 BP.
 DE Human ENZM enzyme gene sequence SeqID89.
 PN WO2003093439-A2.
 PD 13-NOV-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 5.4%; Score 124.8; DB 12; Length 1045;
 Best Local Similarity 49.6%; Pred. No. 8.9e-26;
 RESULT 596
 ID ADC14292 standard; DNA; 1356 BP.
 DE Human enzyme ENZM-45 gene.
 PN WO2003042357-A2.
 PD 22-MAY-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.4%; Score 124.8; DB 10; Length 1356;
 Best Local Similarity 49.6%; Pred. No. 1.1e-25;
 RESULT 597
 ID AAD06844 standard; DNA; 1713 BP.
 DE Human breast cancer specific gene-2 (BCSG-2) #1.
 PN WO200137779-A2.
 PD 31-MAY-2001.
 PA (DIAD-) DIADEXUS INC.
 Query Match 5.4%; Score 124.4; DB 5; Length 1713;
 Best Local Similarity 48.3%; Pred. No. 1.6e-25;
 RESULT 598
 ID ACN91984 standard; DNA; 2844 BP.
 DE Breast cancer related marker, seq id 13134.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 5.4%; Score 124.2; DB 11; Length 2844;
 Best Local Similarity 48.4%; Pred. No. 2.6e-25;
 RESULT 599
 ID ADA10965 standard; cDNA; 1889 BP.
 DE Human cDNA differentially expressed in colon cancer #56.
 PN US2002160382-A1.
 PD 31-OCT-2002.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 5.3%; Score 124; DB 9; Length 1889;
 Best Local Similarity 48.7%; Pred. No. 2.3e-25;
 RESULT 600
 ID ADA11071 standard; cDNA; 1712 BP.
 DE Human cDNA differentially expressed in colon cancer #135.
 PN US2002160382-A1.
 PD 31-OCT-2002.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 5.2%; Score 121.2; DB 9; Length 1712;
 Best Local Similarity 48.1%; Pred. No. 1.5e-24;
 RESULT 601
 ID AAD59155 standard; cDNA; 1712 BP.
 DE Human UDP-glucuronosyltransferase 2B cDNA.
 PN US2003073105-A1.
 PD 17-APR-2003.
 PA (LASE/) LASEK A K W.
 PA (SORN/) SORNASSE T.
 Query Match 5.2%; Score 121.2; DB 10; Length 1712;

Best Local Similarity 48.1%; Pred. No. 1.5e-24;
 RESULT 602
 ID ADR19693 standard; DNA; 1224 BP.
 DE Human drug metabolising enzyme (DME)-14 gene sequence.
 PN WO200226988-A2.
 PD 04-APR-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 5.2%; Score 120.6; DB 7; Length 1224;
 Best Local Similarity 49.8%; Pred. No. 1.8e-24;
 RESULT 603
 ID AAS69712 standard; cDNA; 2111 BP.
 DE DNA encoding novel human diagnostic protein #5516.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.2%; Score 120.6; DB 5; Length 2111;
 Best Local Similarity 49.1%; Pred. No. 2.6e-24;
 RESULT 604
 ID ABX63845 standard; cDNA; 2349 BP.
 DE Human cDNA #845 differentially expressed in activated vascular tissue.
 PN US2002137081-A1.
 PD 26-SEP-2002.
 PA (BAND/) BANDMAN O.
 Query Match 5.2%; Score 119.6; DB 8; Length 2349;
 Best Local Similarity 47.7%; Pred. No. 5.5e-24;
 RESULT 605
 ID ADA11033 standard; cDNA; 2349 BP.
 DE Human cDNA differentially expressed in colon cancer #106.
 PN US2002160382-A1.
 PD 31-OCT-2002.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 5.2%; Score 119.6; DB 9; Length 2349;
 Best Local Similarity 47.7%; Pred. No. 5.5e-24;
 RESULT 606
 ID ABZ23121 standard; DNA; 2351 BP.
 DE Nucleotide sequence of an UDP-glucuronosyltransferase-1.
 PN WO200286074-A2.
 PD 31-OCT-2002.
 PA (MINU) UNIV MINNESOTA.
 PA (STEE/) STEER C J.
 PA (KREN/) KREN B T.
 PA (LINE/) LINEHAN-STIEERS C.
 PA (MCIV/) MCIVOR S R.
 PA (HACK/) HACKETT P B.
 PA (BELU/) BELUR S.
 Query Match 5.2%; Score 119.6; DB 8; Length 2351;
 Best Local Similarity 47.7%; Pred. No. 5.5e-24;
 RESULT 607
 ID ACF62731 standard; DNA; 2351 BP.
 DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:659.
 PN WO2003013534-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 5.2%; Score 119.6; DB 8; Length 2351;
 Best Local Similarity 47.7%; Pred. No. 5.5e-24;
 RESULT 608

ID ADB20846 standard; DNA; 2351 BP.
 DE MRP1 based cancer related nucleic acid SEQ ID NO:659.
 PN WO2003013533-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 5.2%; Score 119.6; DB 8; Length 2351;
 Best Local Similarity 47.7%; Pred. No. 5.5e-24;
 RESULT 609
 ID ADB87935 standard; DNA; 2351 BP.
 DE Human UGT1A1 gene sequence SEQ ID NO:659.
 PN WO2003013536-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 5.2%; Score 119.6; DB 10; Length 2351;
 Best Local Similarity 47.7%; Pred. No. 5.5e-24;
 RESULT 610
 ID ADB96918 standard; DNA; 2351 BP.
 DE Human MDR1 related DNA sequence SEQ ID NO:659.
 PN WO2003013537-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 5.2%; Score 119.6; DB 10; Length 2351;
 Best Local Similarity 47.7%; Pred. No. 5.5e-24;
 RESULT 611
 ID ADB92109 standard; DNA; 2351 BP.
 DE Human MDR1 related DNA sequence SEQ ID NO:659.
 PN WO2003013535-A2.
 PD 20-FEB-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 5.2%; Score 119.6; DB 10; Length 2351;
 Best Local Similarity 47.7%; Pred. No. 5.5e-24;
 RESULT 612
 ID ADH13719 standard; DNA; 1097 BP.
 DE Human ENZM enzyme gene sequence SeqID72.
 PN WO2003093439-A2.
 PD 13-NOV-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 5.1%; Score 119.2; DB 12; Length 1097;
 Best Local Similarity 50.0%; Pred. No. 4.3e-24;
 RESULT 613
 ID ABL68883 standard; DNA; 2422 BP.
 DE Kidney cancer related gene sequence SEQ ID NO:7220.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 5.0%; Score 115.8; DB 6; Length 2422;
 Best Local Similarity 49.1%; Pred. No. 7.6e-23;
 RESULT 614
 ID ABN95608 standard; DNA; 2422 BP.
 DE Gene #2106 used to diagnose liver cancer.
 PN WO200229103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 5.0%; Score 115.8; DB 6; Length 2422;
 Best Local Similarity 49.1%; Pred. No. 7.6e-23;
 RESULT 615
 ID AAQ27369 standard; cDNA; 2351 BP.

DE HUG-Brl.
 PN WO9212987-A1.
 PD 06-AUG-1992.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 Query Match 5.0%; Score 115; DB 2; Length 2351;
 Best Local Similarity 47.5%; Pred. No. 1.3e-22;
 RESULT 616
 ID ADC14256 standard; DNA; 1816 BP.
 DE Human enzyme ENZM-9 gene.
 PN WO2003042357-A2.
 PD 22-MAY-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 4.9%; Score 114.6; DB 10; Length 1816;
 Best Local Similarity 47.1%; Pred. No. 1.4e-22;
 RESULT 617
 ID ADK70323 standard; cDNA; 2366 BP.
 DE Respiratory disease differentially expressed cDNA #59.
 PN WO2003101283-A2.
 PD 11-DEC-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 4.9%; Score 112.8; DB 12; Length 2366;
 Best Local Similarity 48.6%; Pred. No. 5.9e-22;
 RESULT 618
 ID ABX63816 standard; cDNA; 2380 BP.
 DE Human cDNA #816 differentially expressed in activated vascular tissue.
 PN US2002137081-A1.
 PD 26-SEP-2002.
 PA (BAND/) BANDMAN O.
 Query Match 4.9%; Score 112.8; DB 8; Length 2380;
 Best Local Similarity 48.6%; Pred. No. 5.9e-22;
 RESULT 619
 ID ADA11035 standard; cDNA; 2385 BP.
 DE Human cDNA differentially expressed in colon cancer #107.
 PN US2002160382-A1.
 PD 31-OCT-2002.
 PA (LASE/) LASEK A W.
 PA (JONE/) JONES D A.
 Query Match 4.9%; Score 112.8; DB 9; Length 2385;
 Best Local Similarity 48.6%; Pred. No. 5.9e-22;
 RESULT 620
 ID ABA99240 standard; DNA; 2320 BP.
 DE Human UGT1A9 encoding sequence #1.
 PN US2002016293-A1.
 PD 07-FEB-2002.
 PA (RATA/) RATAIN M J.
 PA (INNO/) INNOCENTI F.
 PA (IYER/) IYER L.
 Query Match 4.8%; Score 111.4; DB 6; Length 2320;
 Best Local Similarity 48.4%; Pred. No. 1.5e-21;
 RESULT 621
 ID ABA99241 standard; DNA; 2320 BP.
 DE Human UGT1A9 encoding sequence #2.
 PN US2002016293-A1.
 PD 07-FEB-2002.
 PA (RATA/) RATAIN M J.
 PA (INNO/) INNOCENTI F.
 PA (IYER/) IYER L.

Query Match 4.8%; Score 111.4; DB 6; Length 2320;
 Best Local Similarity 48.4%; Pred. No. 1.5e-21;
 RESULT 622
 ID ABA05198 standard; cDNA; 2320 BP.
 DE Human uridine 5'diphosphate glucuronyltransferase UGT1A9 cDNA #1.
 PN WO200180896-A2.
 PD 01-NOV-2001.
 PA (ARCH-) ARCH DEV CORP.
 Query Match 4.8%; Score 111.4; DB 6; Length 2320;
 Best Local Similarity 48.4%; Pred. No. 1.5e-21;
 RESULT 623
 ID ABA05199 standard; cDNA; 2320 BP.
 DE Human uridine 5'diphosphate glucuronyltransferase UGT1A9 cDNA #2.
 PN WO200180896-A2.
 PD 01-NOV-2001.
 PA (ARCH-) ARCH DEV CORP.
 Query Match 4.8%; Score 111.4; DB 6; Length 2320;
 Best Local Similarity 48.4%; Pred. No. 1.5e-21;
 RESULT 624
 ID AAD30177 standard; DNA; 2320 BP.
 DE Human UDP-glucuronosyl transferase (UGT1A9) gene exon 1.
 PN WO200206523-A2.
 PD 24-JAN-2002.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Query Match 4.8%; Score 111.4; DB 6; Length 2320;
 Best Local Similarity 48.4%; Pred. No. 1.5e-21;
 RESULT 625
 ID ADM72569 standard; DNA; 2585 BP.
 DE Nucleotide sequence of UGT allele UGT1A9*1.
 PN WO2004027088-A2.
 PD 01-APR-2004.
 PA (UYLA-) UNIV LAVAL.
 Query Match 4.8%; Score 111.4; DB 12; Length 2585;
 Best Local Similarity 48.4%; Pred. No. 1.6e-21;
 RESULT 626
 ID ADM72571 standard; DNA; 2585 BP.
 DE Nucleotide sequence of UGT allele UGT1A9*3.
 PN WO2004027088-A2.
 PD 01-APR-2004.
 PA (UYLA-) UNIV LAVAL.
 Query Match 4.8%; Score 111.4; DB 12; Length 2585;
 Best Local Similarity 48.4%; Pred. No. 1.6e-21;
 RESULT 627
 ID ADM72570 standard; DNA; 2585 BP.
 DE Nucleotide sequence of UGT allele UGT1A9*2.
 PN WO2004027088-A2.
 PD 01-APR-2004.
 PA (UYLA-) UNIV LAVAL.
 Query Match 4.8%; Score 111.4; DB 12; Length 2585;
 Best Local Similarity 48.4%; Pred. No. 1.6e-21;
 RESULT 628
 ID AAS81804 standard; cDNA; 2220 BP.
 DE DNA encoding novel human diagnostic protein #17608.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.8%; Score 111.2; DB 5; Length 2220;

Best Local Similarity 79.9%; Pred. No. 1.7e-21;
 RESULT 629
 ID AAS91252 standard; cDNA; 1655 BP.
 DE DNA encoding novel human diagnostic protein #27056.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 4.8%; Score 111; DB 5; Length 1655;
 Best Local Similarity 48.7%; Pred. No. 1.6e-21;
 RESULT 630
 ID ACN89671 standard; DNA; 811 BP.
 DE Breast cancer related marker, seq id 10821.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 4.7%; Score 110; DB 11; Length 811;
 Best Local Similarity 53.9%; Pred. No. 2e-21;
 RESULT 631
 ID ABL11505 standard; cDNA; 1584 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28997.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.4%; Score 101.6; DB 4; Length 1584;
 Best Local Similarity 47.6%; Pred. No. 1e-18;
 RESULT 632
 ID ABL11504 standard; cDNA; 3650 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28994.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.4%; Score 101.6; DB 4; Length 3650;
 Best Local Similarity 47.6%; Pred. No. 1.7e-18;
 RESULT 633
 ID AAQ27370 standard; cDNA; 2368 BP.
 DE HUG-Br2.
 PN WO9212987-A1.
 PD 06-AUG-1992.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 Query Match 4.3%; Score 100.6; DB 2; Length 2368;
 Best Local Similarity 47.9%; Pred. No. 2.6e-18;
 RESULT 634
 ID ABL18781 standard; DNA; 1212 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7816.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.3%; Score 98.8; DB 4; Length 1212;
 Best Local Similarity 49.4%; Pred. No. 5.7e-18;
 RESULT 635
 ID ADS96565 standard; cDNA; 1587 BP.
 DE Drosophila melanogaster protein coding sequence, SEQ ID 186.
 PN WO2004039999-A2.
 PD 13-MAY-2004.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 4.3%; Score 98.8; DB 13; Length 1587;
 Best Local Similarity 47.2%; Pred. No. 6.9e-18;

RESULT 636

ID ABL20593 standard; DNA; 1704 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13252.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 4.3%; Score 98.8; DB 4; Length 1704;
Best Local Similarity 47.2%; Pred. No. 7.2e-18;

RESULT 637

ID ABL18780 standard; DNA; 3212 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7813.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 4.3%; Score 98.8; DB 4; Length 3212;
Best Local Similarity 49.4%; Pred. No. 1.1e-17;

RESULT 638

ID ABL20592 standard; DNA; 4357 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13249.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 4.3%; Score 98.8; DB 4; Length 4357;
Best Local Similarity 47.2%; Pred. No. 1.3e-17;

RESULT 639

ID ABL14299 standard; cDNA; 1458 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37379.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 4.2%; Score 97.6; DB 4; Length 1458;
Best Local Similarity 46.2%; Pred. No. 1.5e-17;

RESULT 640

ID ABL14298 standard; cDNA; 3458 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37376.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 4.2%; Score 97.6; DB 4; Length 3458;
Best Local Similarity 46.2%; Pred. No. 2.6e-17;

RESULT 641

ID ADB58853 standard; DNA; 1593 BP.
DE Toxicity-related gene, SEQ ID 3879.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.

Query Match 4.2%; Score 97; DB 10; Length 1593;
Best Local Similarity 47.7%; Pred. No. 2.4e-17;

RESULT 642

ID ADB53570 standard; DNA; 1593 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4112.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.

Query Match 4.2%; Score 97; DB 10; Length 1593;
Best Local Similarity 47.7%; Pred. No. 2.4e-17;

RESULT 643

ID ABT42362 standard; DNA; 1593 BP.
 DE Toxicity modelling related rat gene SEQ ID No 2064.
 PN WO200295000-A2.
 PD 28-NOV-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 4.2%; Score 97; DB 10; Length 1593;
 Best Local Similarity 47.7%; Pred. No. 2.4e-17;
 RESULT 644
 ID ADP72524 standard; DNA; 1593 BP.
 DE Renal toxin progression gene marker #1113.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 4.2%; Score 97; DB 12; Length 1593;
 Best Local Similarity 47.7%; Pred. No. 2.4e-17;
 RESULT 645
 ID AAZ45118 standard; DNA; 735 BP.
 DE UDP-glucuronosyltransferase 1 (UGT1) exons 2-5 nucleotide sequence.
 PN WO9957322-A2.
 PD 11-NOV-1999.
 PA (AXYS-) AXYS PHARM INC.
 Query Match 4.1%; Score 95.6; DB 3; Length 735;
 Best Local Similarity 50.2%; Pred. No. 3.7e-17;
 RESULT 646
 ID ADP72545 standard; DNA; 1927 BP.
 DE Renal toxin progression gene marker #1134.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 4.1%; Score 95.4; DB 12; Length 1927;
 Best Local Similarity 47.5%; Pred. No. 8.1e-17;
 RESULT 647
 ID ABL11511 standard; cDNA; 1560 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29015.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.0%; Score 93.4; DB 4; Length 1560;
 Best Local Similarity 50.8%; Pred. No. 2.8e-16;
 RESULT 648
 ID ABL11510 standard; cDNA; 3828 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29012.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.0%; Score 93.4; DB 4; Length 3828;
 Best Local Similarity 50.8%; Pred. No. 5e-16;
 RESULT 649
 ID ACN45086 standard; DNA; 54493 BP.
 DE Human genomic sequence hCG37578.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 4.0%; Score 93.2; DB 11; Length 54493;
 Best Local Similarity 79.1%; Pred. No. 3.4e-15;
 RESULT 650
 ID ABL07443 standard; cDNA; 1652 BP.

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16811.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.0%; Score 93; DB 4; Length 1652;
 Best Local Similarity 49.7%; Pred. No. 3.8e-16;
 RESULT 651
 ID ABL07442 standard; cDNA; 3991 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16808.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.0%; Score 93; DB 4; Length 3991;
 Best Local Similarity 49.7%; Pred. No. 6.8e-16;
 RESULT 652
 ID ABL15252 standard; cDNA; 14112 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40238.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 4.0%; Score 93; DB 4; Length 14112;
 Best Local Similarity 49.7%; Pred. No. 1.6e-15;
 RESULT 653
 ID ABT09061 standard; DNA; 662 BP.
 DE Phase-1 Rat CT gene SEQ ID No 149.
 PN WO200266682-A2.
 PD 29-AUG-2002.
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 Query Match 4.0%; Score 92.8; DB 6; Length 662;
 Best Local Similarity 50.4%; Pred. No. 2.4e-16;
 RESULT 654
 ID ADR91345 standard; cDNA; 662 BP.
 DE Spleen necrosis predictive cDNA sequence, SEQ ID No 301.
 PN WO2004083402-A2.
 PD 30-SEP-2004.
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 Query Match 4.0%; Score 92.8; DB 13; Length 662;
 Best Local Similarity 50.4%; Pred. No. 2.4e-16;
 RESULT 655
 ID ABT09603 standard; DNA; 642 BP.
 DE Phase-1 Rat CT gene SEQ ID No 691.
 PN WO200266682-A2.
 PD 29-AUG-2002.
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 Query Match 4.0%; Score 91.8; DB 6; Length 642;
 Best Local Similarity 50.4%; Pred. No. 4.6e-16;
 RESULT 656
 ID ADG45772 standard; DNA; 642 BP.
 DE Liver inflammatory predictive gene related DNA sequence.
 PN WO2003095624-A2.
 PD 20-NOV-2003.
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 Query Match 4.0%; Score 91.8; DB 12; Length 642;
 Best Local Similarity 50.4%; Pred. No. 4.6e-16;
 RESULT 657
 ID ADH23038 standard; DNA; 642 BP.
 DE Partial DNA sequence of a rat kidney toxicity predictive gene (366).

PN WO2003100030-A2.
 PD 04-DEC-2003.
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 Query Match 4.0%; Score 91.8; DB 12; Length 642;
 Best Local Similarity 50.4%; Pred. No. 4.6e-16;
 RESULT 658
 ID ABT09349 standard; DNA; 662 BP.
 DE Phase-1 Rat CT gene SEQ ID No 437.
 PN WO200266682-A2.
 PD 29-AUG-2002.
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 Query Match 3.9%; Score 91.6; DB 6; Length 662;
 Best Local Similarity 50.5%; Pred. No. 5.4e-16;
 RESULT 659
 ID ABL26823 standard; DNA; 1648 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31942.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.9%; Score 91; DB 4; Length 1648;
 Best Local Similarity 46.0%; Pred. No. 1.5e-15;
 RESULT 660
 ID AAD57526 standard; cDNA; 2526 BP.
 DE Human enzyme (ENZM) cDNA #38.
 PN WO2003052075-A2.
 PD 26-JUN-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 3.9%; Score 90.6; DB 9; Length 2526;
 Best Local Similarity 49.6%; Pred. No. 2.6e-15;
 RESULT 661
 ID ADH13757 standard; DNA; 2602 BP.
 DE Human ENZM enzyme gene sequence SeqID110.
 PN WO2003093439-A2.
 PD 13-NOV-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 3.8%; Score 89.2; DB 12; Length 2602;
 Best Local Similarity 49.3%; Pred. No. 7e-15;
 RESULT 662
 ID ABL27914 standard; DNA; 5278 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35215.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.8%; Score 88.8; DB 4; Length 5278;
 Best Local Similarity 47.6%; Pred. No. 1.5e-14;
 RESULT 663
 ID ADP72573 standard; DNA; 2484 BP.
 DE Renal toxin progression gene marker #1162.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.8%; Score 88.2; DB 12; Length 2484;
 Best Local Similarity 47.8%; Pred. No. 1.4e-14;
 RESULT 664
 ID AAD57521 standard; cDNA; 2491 BP.
 DE Human enzyme (ENZM) cDNA #33.
 PN WO2003052075-A2.

PD 26-JUN-2003.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 3.8%; Score 88; DB 9; Length 2491;

Best Local Similarity 49.8%; Pred. No. 1.6e-14;

RESULT 665

ID ABL11161 standard; cDNA; 1595 BP.

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27965.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 3.8%; Score 87.4; DB 4; Length 1595;

Best Local Similarity 45.9%; Pred. No. 1.7e-14;

RESULT 666

ID ABX44475 standard; cDNA; 419 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #9640.

PN US2002137139-A1.

PD 26-SEP-2002.

PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.

PA (WARR/) WARREN W C.

Query Match 3.7%; Score 86.2; DB 8; Length 419;

Best Local Similarity 55.6%; Pred. No. 1.6e-14;

RESULT 667

ID ABL01468 standard; DNA; 874 BP.

DE Murine apoptosis related DNA sequence #133.

PN DE10126344-A1.

PD 24-JAN-2002.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

Query Match 3.7%; Score 86.2; DB 6; Length 874;

Best Local Similarity 49.2%; Pred. No. 2.7e-14;

RESULT 668

ID ABL30082 standard; DNA; 3716 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41719.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 3.7%; Score 85.2; DB 4; Length 3716;

Best Local Similarity 46.0%; Pred. No. 1.4e-13;

RESULT 669

ID ABL28713 standard; DNA; 1572 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37612.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 3.6%; Score 82.6; DB 4; Length 1572;

Best Local Similarity 48.1%; Pred. No. 4.7e-13;

RESULT 670

ID ABL28712 standard; DNA; 3572 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37609.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 3.6%; Score 82.6; DB 4; Length 3572;

Best Local Similarity 48.1%; Pred. No. 8.1e-13;

RESULT 671

ID ABL11160 standard; cDNA; 4016 BP.

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27962.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 3.5%; Score 80.8; DB 4; Length 4016;
Best Local Similarity 47.9%; Pred. No. 3e-12;

RESULT 672

ID ABL29221 standard; DNA; 1593 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39136.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 3.5%; Score 80.6; DB 4; Length 1593;
Best Local Similarity 49.5%; Pred. No. 1.9e-12;

RESULT 673

ID ABL29220 standard; DNA; 3659 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39133.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 3.5%; Score 80.6; DB 4; Length 3659;
Best Local Similarity 49.5%; Pred. No. 3.3e-12;

RESULT 674

ID ABL28205 standard; DNA; 1413 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 36088.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 3.4%; Score 79.4; DB 4; Length 1413;
Best Local Similarity 48.4%; Pred. No. 3.9e-12;

RESULT 675

ID ABL27915 standard; DNA; 2820 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35218.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 3.4%; Score 79.4; DB 4; Length 2820;
Best Local Similarity 49.0%; Pred. No. 6.2e-12;

RESULT 676

ID ABT09604 standard; DNA; 678 BP.
DE Phase-1 Rat CT gene SEQ ID No 692.
PN WO200266682-A2.
PD 29-AUG-2002.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

Query Match 3.4%; Score 78.6; DB 6; Length 678;
Best Local Similarity 49.4%; Pred. No. 4.2e-12;

RESULT 677

ID ABL26822 standard; DNA; 5205 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31939.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 3.4%; Score 77.8; DB 4; Length 5205;
Best Local Similarity 58.4%; Pred. No. 2.8e-11;

RESULT 678

ID ABX48695 standard; cDNA; 426 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #13860.

PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 3.3%; Score 76.8; DB 8; Length 426;
 Best Local Similarity 49.0%; Pred. No. 1.1e-11;
 RESULT 679
 ID ABX44899 standard; cDNA; 418 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #10064.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 3.3%; Score 75.8; DB 8; Length 418;
 Best Local Similarity 52.8%; Pred. No. 2.1e-11;
 RESULT 680
 ID ABK63527 standard; cDNA; 603 BP.
 DE Rat sequence differentially expressed in response to a hepatotoxin #1434.
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.2%; Score 74.6; DB 6; Length 603;
 Best Local Similarity 48.3%; Pred. No. 6.1e-11;
 RESULT 681
 ID ADP72781 standard; DNA; 603 BP.
 DE Renal toxin progression gene marker #1370.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.2%; Score 74.6; DB 12; Length 603;
 Best Local Similarity 48.3%; Pred. No. 6.1e-11;
 RESULT 682
 ID ABL78475 standard; cDNA; 582 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:1453.
 PN WO200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 3.2%; Score 74; DB 6; Length 582;
 Best Local Similarity 61.3%; Pred. No. 9e-11;
 RESULT 683
 ID AAS91382 standard; cDNA; 2406 BP.
 DE DNA encoding novel human diagnostic protein #27186.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 3.2%; Score 73.4; DB 5; Length 2406;
 Best Local Similarity 48.4%; Pred. No. 3.5e-10;
 RESULT 684
 ID AAL19612 standard; cDNA; 293 BP.
 DE Human breast cancer expressed polynucleotide 12069.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 3.1%; Score 72; DB 4; Length 293;
 Best Local Similarity 60.9%; Pred. No. 2.3e-10;
 RESULT 685
 ID AAL10032 standard; cDNA; 439 BP.
 DE Human breast cancer expressed polynucleotide 2489.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 3.1%; Score 72; DB 4; Length 439;
 Best Local Similarity 60.9%; Pred. No. 2.9e-10;
 RESULT 686
 ID ACN80231 standard; DNA; 450 BP.
 DE Breast cancer related marker, seq id 1381.
 PN US2003099974-A1.
 PD 29-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.1%; Score 72; DB 11; Length 450;
 Best Local Similarity 60.9%; Pred. No. 3e-10;
 RESULT 687
 ID ABK63526 standard; cDNA; 601 BP.
 DE Rat sequence differentially expressed in response to a hepatotoxin #1433.
 PN WO200210453-A2.
 PD 07-FEB-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.1%; Score 70.8; DB 6; Length 601;
 Best Local Similarity 48.1%; Pred. No. 8.3e-10;
 RESULT 688
 ID ADP72780 standard; DNA; 601 BP.
 DE Renal toxin progression gene marker #1369.
 PN WO2004048598-A2.
 PD 10-JUN-2004.
 PA (GENE-) GENE LOGIC INC.
 Query Match 3.1%; Score 70.8; DB 12; Length 601;
 Best Local Similarity 48.1%; Pred. No. 8.3e-10;
 RESULT 689
 ID ABL11455 standard; cDNA; 1680 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28847.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.0%; Score 69.4; DB 4; Length 1680;
 Best Local Similarity 45.5%; Pred. No. 4.3e-09;
 RESULT 690
 ID ABL11471 standard; cDNA; 1782 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28895.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.0%; Score 69.4; DB 4; Length 1782;
 Best Local Similarity 44.3%; Pred. No. 4.5e-09;
 RESULT 691
 ID ABL11454 standard; cDNA; 3741 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28844.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.0%; Score 69.4; DB 4; Length 3741;

Best Local Similarity 45.5%; Pred. No. 7.3e-09;
 RESULT 692
 ID ABL11470 standard; cDNA; 3849 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28892.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.0%; Score 69.4; DB 4; Length 3849;
 Best Local Similarity 44.3%; Pred. No. 7.4e-09;
 RESULT 693
 ID ABX36904 standard; cDNA; 350 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #2069.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 3.0%; Score 69.2; DB 8; Length 350;
 Best Local Similarity 58.1%; Pred. No. 1.7e-09;
 RESULT 694
 ID ABX36905 standard; cDNA; 381 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #2070.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 3.0%; Score 69.2; DB 8; Length 381;
 Best Local Similarity 58.1%; Pred. No. 1.8e-09;
 RESULT 695
 ID ABL08183 standard; cDNA; 1491 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19031.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.0%; Score 69.2; DB 4; Length 1491;
 Best Local Similarity 56.0%; Pred. No. 4.6e-09;
 RESULT 696
 ID ABL08182 standard; cDNA; 3784 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19028.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.0%; Score 69.2; DB 4; Length 3784;
 Best Local Similarity 56.0%; Pred. No. 8.4e-09;
 RESULT 697
 ID ABL29264 standard; DNA; 3595 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39265.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.0%; Score 68.6; DB 4; Length 3595;
 Best Local Similarity 48.6%; Pred. No. 1.2e-08;
 RESULT 698
 ID ABL29265 standard; DNA; 1539 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39268.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.9%; Score 68; DB 4; Length 1539;
Best Local Similarity 51.4%; Pred. No. 1.1e-08;

RESULT 699

ID AAS81103 standard; cDNA; 2602 BP.
DE DNA encoding novel human diagnostic protein #16907.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 2.9%; Score 67.2; DB 5; Length 2602;
Best Local Similarity 57.7%; Pred. No. 2.6e-08;

RESULT 700

ID AAS91381 standard; cDNA; 2602 BP.
DE DNA encoding novel human diagnostic protein #27185.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 2.9%; Score 67.2; DB 5; Length 2602;
Best Local Similarity 57.7%; Pred. No. 2.6e-08;

RESULT 701

ID AAS92577 standard; cDNA; 2602 BP.
DE DNA encoding novel human diagnostic protein #28381.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match 2.9%; Score 67.2; DB 5; Length 2602;
Best Local Similarity 57.7%; Pred. No. 2.6e-08;

RESULT 702

ID ABX47071 standard; cDNA; 416 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12236.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.

Query Match 2.9%; Score 66.8; DB 8; Length 416;
Best Local Similarity 55.6%; Pred. No. 1e-08;

RESULT 703

ID ABL26825 standard; DNA; 1931 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31948.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.9%; Score 66.2; DB 4; Length 1931;
Best Local Similarity 48.1%; Pred. No. 4.3e-08;

RESULT 704

ID ABL18375 standard; DNA; 1188 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6598.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 66; DB 4; Length 1188;
Best Local Similarity 47.9%; Pred. No. 3.5e-08;

RESULT 705

ID ABL18374 standard; DNA; 3188 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6595.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 66; DB 4; Length 3188;
Best Local Similarity 47.9%; Pred. No. 6.8e-08;

RESULT 706

ID ABL19473 standard; DNA; 1672 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9892.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 65.8; DB 4; Length 1672;
Best Local Similarity 45.8%; Pred. No. 5.1e-08;

RESULT 707

ID ABL19472 standard; DNA; 3751 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9889.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 65.8; DB 4; Length 3751;
Best Local Similarity 45.8%; Pred. No. 8.7e-08;

RESULT 708

ID ABL18869 standard; DNA; 1488 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8080.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 65.4; DB 4; Length 1488;
Best Local Similarity 60.3%; Pred. No. 6.2e-08;

RESULT 709

ID ABL26827 standard; DNA; 1584 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31954.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 65.4; DB 4; Length 1584;
Best Local Similarity 60.3%; Pred. No. 6.5e-08;

RESULT 710

ID ABX74515 standard; cDNA; 1977 BP.
DE Human cDNA sequence #58 down-regulated in CC-RCC patients.
PN WO200279411-A2.
PD 10-OCT-2002.
PA (VAND-) VAN ANDEL INST.

Query Match 2.8%; Score 65.4; DB 10; Length 1977;
Best Local Similarity 58.5%; Pred. No. 7.5e-08;

RESULT 711

ID ABL16660 standard; DNA; 3613 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1453.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 65.4; DB 4; Length 3613;
Best Local Similarity 60.3%; Pred. No. 1.1e-07;

RESULT 712

ID ABL26826 standard; DNA; 4082 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO.31951.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.8%; Score 65.4; DB 4; Length 4082;
 Best Local Similarity 60.3%; Pred. No. 1.2e-07;
 RESULT 713
 ID ABL18868 standard; DNA; 4082 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8077.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.8%; Score 65.4; DB 4; Length 4082;
 Best Local Similarity 60.3%; Pred. No. 1.2e-07;
 RESULT 714
 ID ABL16191 standard; DNA; 1623 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 46.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.8%; Score 64.6; DB 4; Length 1623;
 Best Local Similarity 52.4%; Pred. No. 1.1e-07;
 RESULT 715
 ID ABL16190 standard; DNA; 3683 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 43.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.8%; Score 64.6; DB 4; Length 3683;
 Best Local Similarity 52.4%; Pred. No. 2e-07;
 RESULT 716
 ID AAA87473 standard; DNA; 259 BP.
 DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:397.
 PN WO200044902-A2.
 PD 03-AUG-2000.
 PA (SEAR) SEARLE & CO G D.
 Query Match 2.8%; Score 64.4; DB 3; Length 259;
 Best Local Similarity 53.1%; Pred. No. 3.9e-08;
 RESULT 717
 ID AAI17431 standard; DNA; 500 BP.
 DE Probe #7364 for gene expression analysis in human cervical cell sample.
 PN WO200157278-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.8%; Score 63.8; DB 4; Length 500;
 Best Local Similarity 60.8%; Pred. No. 9e-08;
 RESULT 718
 ID ABA62357 standard; DNA; 500 BP.
 DE Human foetal liver single exon nucleic acid probe #10662.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.8%; Score 63.8; DB 4; Length 500;
 Best Local Similarity 60.8%; Pred. No. 9e-08;
 RESULT 719
 ID AAI42337 standard; DNA; 500 BP.

DE Probe #11023 used to measure gene expression in human placenta sample.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.8%; Score 63.8; DB 4; Length 500;
 Best Local Similarity 60.8%; Pred. No. 9e-08;
 RESULT 720
 ID ABA29697 standard; DNA; 500 BP.
 DE Probe #8163 for gene expression analysis in human heart cell sample.
 PN WO200157274-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.8%; Score 63.8; DB 4; Length 500;
 Best Local Similarity 60.8%; Pred. No. 9e-08;
 RESULT 721
 ID AAK36579 standard; DNA; 500 BP.
 DE Human bone marrow expressed single exon probe SEQ ID NO: 11136.
 PN WO200157276-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.8%; Score 63.8; DB 4; Length 500;
 Best Local Similarity 60.8%; Pred. No. 9e-08;
 RESULT 722
 ID AAK10692 standard; DNA; 500 BP.
 DE Human brain expressed single exon probe SEQ ID NO: 10683.
 PN WO200157275-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.8%; Score 63.8; DB 4; Length 500;
 Best Local Similarity 60.8%; Pred. No. 9e-08;
 RESULT 723
 ID ABS36232 standard; DNA; 500 BP.
 DE Human liver single exon probe, SEQ ID No 11222.
 PN WO200157273-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.8%; Score 63.8; DB 4; Length 500;
 Best Local Similarity 60.8%; Pred. No. 9e-08;
 RESULT 724
 ID AAZ95197 standard; DNA; 689 BP.
 DE Human UGT2B4 exon 5 nucleotide sequence.
 PN WO200006776-A1.
 PD 10-FEB-2000.
 PA (AXYS-) AXYS PHARM INC.
 Query Match 2.8%; Score 63.8; DB 3; Length 689;
 Best Local Similarity 60.8%; Pred. No. 1.1e-07;
 RESULT 725
 ID ABL15269 standard; cDNA; 1521 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40289.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.8%; Score 63.8; DB 4; Length 1521;
 Best Local Similarity 46.3%; Pred. No. 1.9e-07;
 RESULT 726
 ID ABL15268 standard; cDNA; 3576 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40286.

PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.8%; Score 63.8; DB 4; Length 3576;
Best Local Similarity 46.3%; Pred. No. 3.3e-07;

RESULT 727

ID ABX38071 standard; cDNA; 370 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3236.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.

Query Match 2.7%; Score 63.6; DB 8; Length 370;
Best Local Similarity 54.8%; Pred. No. 8.5e-08;

RESULT 728

ID ABX36135 standard; cDNA; 378 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #1300.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.

Query Match 2.7%; Score 63.4; DB 8; Length 378;
Best Local Similarity 56.5%; Pred. No. 9.9e-08;

RESULT 729

ID ADT97393 standard; cDNA; 396 BP.
DE Colon cancer associated human cDNA sequence #2900.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 63.4; DB 11; Length 396;
Best Local Similarity 53.1%; Pred. No. 1e-07;

RESULT 730

ID ABK12423 standard; DNA; 21000 BP.
DE cDNA encoding human drug-metabolising enzyme.
PN WO200218554-A2.
PD 07-MAR-2002.
PA (APPL-) APPLERA CORP.

Query Match 2.7%; Score 63.4; DB 6; Length 21000;
Best Local Similarity 58.9%; Pred. No. 1.4e-06;

RESULT 731

ID AAZ07208 standard; cDNA; 391 BP.
DE Human lung tumour protein LT86-5 cDNA sequence.
PN WO9938973-A2.
PD 05-AUG-1999.
PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 62.4; DB 2; Length 391;
Best Local Similarity 54.3%; Pred. No. 2e-07;

RESULT 732

ID AAC79066 standard; cDNA; 391 BP.
DE Human lung tumour-specific cDNA #21.
PN WO200060077-A2.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 62.4; DB 3; Length 391;
Best Local Similarity 54.3%; Pred. No. 2e-07;

RESULT 733

ID AAD23141 standard; cDNA; 391 BP.
DE Human lung tumour-specific protein LT86-5 cDNA.
PN WO200172295-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 62.4; DB 4; Length 391;
Best Local Similarity 54.3%; Pred. No. 2e-07;

RESULT 734

ID ADD67078 standard; cDNA; 391 BP.
DE Human lung tumour-specific cDNA sequence, SEQ ID No 21.
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 62.4; DB 10; Length 391;
Best Local Similarity 54.3%; Pred. No. 2e-07;

RESULT 735

ID ADE87583 standard; cDNA; 391 BP.
DE Human lung tumour antigen cDNA #21.
PN US2003118599-A1.
PD 26-JUN-2003.
PA (CORI-) CORIXA CORP.

Query Match 2.7%; Score 62.4; DB 10; Length 391;
Best Local Similarity 54.3%; Pred. No. 2e-07;

RESULT 736

ID ABX45859 standard; cDNA; 417 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11024.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.

Query Match 2.7%; Score 62.4; DB 8; Length 417;
Best Local Similarity 57.8%; Pred. No. 2.1e-07;

RESULT 737

ID ABL17155 standard; DNA; 1443 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2938.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.7%; Score 62.2; DB 4; Length 1443;
Best Local Similarity 45.4%; Pred. No. 5.5e-07;

RESULT 738

ID AAZ95204 standard; DNA; 1591 BP.
DE Human UGT2B7 exon 4 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.

Query Match 2.7%; Score 62.2; DB 3; Length 1591;
Best Local Similarity 60.2%; Pred. No. 5.9e-07;

RESULT 739

ID ABL17154 standard; DNA; 3495 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2935.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.7%; Score 62.2; DB 4; Length 3495;
Best Local Similarity 45.4%; Pred. No. 9.9e-07;
RESULT 740
ID ADB58891 standard; DNA; 2301 BP.
DE Toxicity-related gene, SEQ ID 3917.
PN WO2003064624-A2.
PD 07-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 62; DB 10; Length 2301;
Best Local Similarity 46.7%; Pred. No. 8.6e-07;
RESULT 741
ID ADB53607 standard; DNA; 2301 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4149.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 2.7%; Score 62; DB 10; Length 2301;
Best Local Similarity 46.7%; Pred. No. 8.6e-07;
RESULT 742
ID ABZ83776 standard; cDNA; 1024 BP.
DE Toxicologically relevant human nucleotide sequence #935.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 2.7%; Score 61.8; DB 10; Length 1024;
Best Local Similarity 48.2%; Pred. No. 5.7e-07;
RESULT 743
ID ABL07575 standard; cDNA; 1527 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17207.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.7%; Score 61.8; DB 4; Length 1527;
Best Local Similarity 46.1%; Pred. No. 7.5e-07;
RESULT 744
ID ABL07574 standard; cDNA; 4647 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17204.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.7%; Score 61.8; DB 4; Length 4647;
Best Local Similarity 46.1%; Pred. No. 1.6e-06;
RESULT 745
ID ABL16192 standard; DNA; 3679 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 49.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 2.6%; Score 61.4; DB 4; Length 3679;
Best Local Similarity 51.7%; Pred. No. 1.8e-06;
RESULT 746
ID ABL30083 standard; DNA; 1500 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41722.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 2.6%; Score 60.4; DB 4; Length 1500;
Best Local Similarity 47.8%; Pred. No. 1.9e-06;

RESULT 747

ID ABX37848 standard; cDNA; 196 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #3013.

PN US2002137139-A1.

PD 26-SEP-2002.

PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.

PA (WARR/) WARREN W C.

Query Match 2.6%; Score 60.2; DB 8; Length 196;

Best Local Similarity 57.8%; Pred. No. 5.8e-07;

RESULT 748

ID AAI26647 standard; DNA; 220 BP.

DE Probe #16580 for gene expression analysis in human cervical cell sample.

PN WO200157278-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.6%; Score 60; DB 4; Length 220;

Best Local Similarity 60.4%; Pred. No. 7.1e-07;

RESULT 749

ID ABA74889 standard; DNA; 220 BP.

DE Human foetal liver single exon nucleic acid probe #23194.

PN WO200157277-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.6%; Score 60; DB 4; Length 220;

Best Local Similarity 60.4%; Pred. No. 7.1e-07;

RESULT 750

ID AAI55416 standard; DNA; 220 BP.

DE Probe #24102 used to measure gene expression in human placenta sample.

PN WO200157272-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.6%; Score 60; DB 4; Length 220;

Best Local Similarity 60.4%; Pred. No. 7.1e-07;

RESULT 751

ID ABA39585 standard; DNA; 220 BP.

DE Probe #18051 for gene expression analysis in human heart cell sample.

PN WO200157274-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.6%; Score 60; DB 4; Length 220;

Best Local Similarity 60.4%; Pred. No. 7.1e-07;

RESULT 752

ID AAK49539 standard; DNA; 220 BP.

DE Human bone marrow expressed single exon probe SEQ ID NO: 24096.

PN WO200157276-A2.

PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.6%; Score 60; DB 4; Length 220;

Best Local Similarity 60.4%; Pred. No. 7.1e-07;

RESULT 753

ID AAK23383 standard; DNA; 220 BP.

DE Human brain expressed single exon probe SEQ ID NO: 23374.

PN WO200157275-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.6%; Score 60; DB 4; Length 220;
 Best Local Similarity 60.4%; Pred. No. 7.1e-07;
 RESULT 754
 ID ABS49158 standard; DNA; 220 BP.
 DE Human liver single exon probe, SEQ ID No 24148.
 PN WO200157273-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.6%; Score 60; DB 4; Length 220;
 Best Local Similarity 60.4%; Pred. No. 7.1e-07;
 RESULT 755
 ID ABL11493 standard; cDNA; 1668 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28961.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.6%; Score 59.6; DB 4; Length 1668;
 Best Local Similarity 50.9%; Pred. No. 3.6e-06;
 RESULT 756
 ID ABL11492 standard; cDNA; 3740 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28958.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.6%; Score 59.6; DB 4; Length 3740;
 Best Local Similarity 50.9%; Pred. No. 6.2e-06;
 RESULT 757
 ID ABN85391 standard; DNA; 1606 BP.
 DE Human NOV13, glucuronosyltransferase-like protein, coding sequence.
 PN WO200255704-A2.
 PD 18-JUL-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.6%; Score 59.4; DB 6; Length 1606;
 Best Local Similarity 48.6%; Pred. No. 4e-06;
 RESULT 758
 ID ADI16615 standard; cDNA; 1606 BP.
 DE Human NOVX cDNA to treat human pathological conditions SeqID151.
 PN WO200268649-A2.
 PD 06-SEP-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 2.6%; Score 59.4; DB 6; Length 1606;
 Best Local Similarity 48.6%; Pred. No. 4e-06;
 RESULT 759.
 ID ADN42269 standard; cDNA; 1606 BP.
 DE Human cDNA encoding NOV 40.
 PN US2004033493-A1.
 PD 19-FEB-2004.
 PA (TCHE/) TCHERNEV V T.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PATT/) PATTURAJAN M.
 PA (SHIM/) SHIMKETS R A.
 PA (LILL/) LI L.
 PA (GANG/) GANGOLLI E A.

PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.

Query Match 2.6%; Score 59.4; DB 12; Length 1606;
Best Local Similarity 48.6%; Pred. No. 4e-06;.

RESULT 760

ID ABA63293 standard; DNA; 589 BP.
DE Human foetal liver single exon nucleic acid probe #11598.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.5%; Score 59; DB 4; Length 589;
Best Local Similarity 59.1%; Pred. No. 2.7e-06;

RESULT 761

ID ABS37187 standard; DNA; 589 BP.
DE Human liver single exon probe, SEQ ID No 12177.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.5%; Score 59; DB 4; Length 589;
Best Local Similarity 59.1%; Pred. No. 2.7e-06;

RESULT 762

ID ADT97647 standard; cDNA; 432 BP.
DE Colon cancer associated human cDNA sequence #3154.
PN US2003087818-A1.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.

Query Match 2.5%; Score 58.2; DB 11; Length 432;
Best Local Similarity 51.0%; Pred. No. 3.9e-06;

RESULT 763

ID AAD57513 standard; cDNA; 1465 BP.
DE Human enzyme (ENZM) cDNA #25.
PN WO2003052075-A2.
PD 26-JUN-2003.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 2.5%; Score 58.2; DB 9; Length 1465;
Best Local Similarity 52.6%; Pred. No. 8.7e-06;

RESULT 764

ID ABL08287 standard; cDNA; 2036 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19343.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.5%; Score 57.4; DB 4; Length 2036;

Best Local Similarity 44.9%; Pred. No. 1.9e-05;
 RESULT 765
 ID ABL08286 standard; cDNA; 4386 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19340.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.5%; Score 57.4; DB 4; Length 4386;
 Best Local Similarity 44.9%; Pred. No. 3.1e-05;
 RESULT 766
 ID AAT10106 standard; cDNA to mRNA; 1731 BP.
 DE Maize UDP-glucose indol-3-yl:acetyl:glucosyl transferase sequence.
 PN WO9600291-A1.
 PD 04-JAN-1996.
 PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
 Query Match 2.4%; Score 56.8; DB 2; Length 1731;
 Best Local Similarity 60.3%; Pred. No. 2.5e-05;
 RESULT 767
 ID AAH51495 standard; DNA; 983 BP.
 DE Human UGT2B4 related DNA containing a biallelic polymorphism SEQ ID 386.
 PN WO200058508-A2.
 PD 05-OCT-2000.
 PA (GEST) GENSET.
 Query Match 2.4%; Score 56.2; DB 3; Length 983;
 Best Local Similarity 53.4%; Pred. No. 2.6e-05;
 RESULT 768
 ID ABL26824 standard; DNA; 4966 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 31945.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.4%; Score 56.2; DB 4; Length 4966;
 Best Local Similarity 50.2%; Pred. No. 7.7e-05;
 RESULT 769
 ID AAC03286 standard; cDNA; 350 BP.
 DE Human secreted protein 5' EST, SEQ ID NO: 3284.
 PN EP1033401-A2.
 PD 06-SEP-2000.
 PA (GEST) GENSET.
 Query Match 2.4%; Score 55.8; DB 3; Length 350;
 Best Local Similarity 53.7%; Pred. No. 1.7e-05;
 RESULT 770
 ID ABZ83269 standard; cDNA; 1024 BP.
 DE Toxicologically relevant human nucleotide sequence #428.
 PN WO2003016500-A2.
 PD 27-FEB-2003.
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 Query Match 2.4%; Score 55.6; DB 10; Length 1024;
 Best Local Similarity 48.7%; Pred. No. 4.1e-05;
 RESULT 771
 ID ABA75736 standard; DNA; 203 BP.
 DE Human foetal liver single exon nucleic acid probe #24041.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 2.4%; Score 55.2; DB 4; Length 203;
 Best Local Similarity 58.5%; Pred. No. 1.8e-05;

RESULT 772

ID ABS50023 standard; DNA; 203 BP.
DE Human liver single exon probe, SEQ ID No 25013.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.

Query Match 2.4%; Score 55.2; DB 4; Length 203;
Best Local Similarity 58.5%; Pred. No. 1.8e-05;

RESULT 773

ID AAZ95210 standard; DNA; 1602 BP.
DE Human UGT2B15 exon 4 nucleotide sequence.
PN WO200006776-A1.
PD 10-FEB-2000.
PA (AXYS-) AXYS PHARM INC.

Query Match 2.4%; Score 55; DB 3; Length 1602;
Best Local Similarity 61.5%; Pred. No. 8.3e-05;

RESULT 774

ID AAD55028 standard; DNA; 1380 BP.
DE Alstroemeria UDP-glucosyltransferase homologue gene, k7.
PN WO2002101013-A2.
PD 19-DEC-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PRAB/) PRABHU V.

Query Match 2.3%; Score 54.2; DB 10; Length 1380;
Best Local Similarity 58.3%; Pred. No. 0.00013;

RESULT 775

ID ABL28204 standard; DNA; 3642 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 36085.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 2.3%; Score 54.2; DB 4; Length 3642;
Best Local Similarity 58.3%; Pred. No. 0.00025;

RESULT 776

ID ADJ12064 standard; DNA; 531 BP.
DE Maize cDNA modulated by post-transcriptional gene silencing SeqID 700.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZE BROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.

Query Match 2.3%; Score 53.8; DB 11; Length 531;
Best Local Similarity 57.4%; Pred. No. 9.1e-05;

RESULT 777

ID AAD55029 standard; DNA; 1380 BP.
DE Alstroemeria UDP-glucosyltransferase homologue gene, e12.
PN WO2002101013-A2.
PD 19-DEC-2002.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PA (PRAB/) PRABHU V.

Query Match 2.3%; Score 53.8; DB 10; Length 1380;
Best Local Similarity 57.4%; Pred. No. 0.00017;

RESULT 778

ID ACH80037 standard; DNA; 577 BP.

DE Human genome derived single exon probe #13232.

PN US2003194704-A1.

PD 16-OCT-2003.

PA (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

Query Match 2.3%; Score 53.4; DB 12; Length 577;
Best Local Similarity 51.9%; Pred. No. 0.00013;

RESULT 779

ID AAQ33026 standard; DNA; 775 BP.

DE Exons 3-4 from the UGT1 gene locus.

PN WO9212987-A1.

PD 06-AUG-1992.

PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

Query Match 2.3%; Score 53.4; DB 2; Length 775;
Best Local Similarity 51.9%; Pred. No. 0.00015;

RESULT 780

ID AAD30179 standard; DNA; 784 BP.

DE Human UDP-glucuronosyl transferase (UGT1A) gene exon 4.

PN WO200206523-A2.

PD 24-JAN-2002.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

Query Match 2.3%; Score 53.4; DB 6; Length 784;
Best Local Similarity 51.9%; Pred. No. 0.00016;

RESULT 781

ID ABL16193 standard; DNA; 1620 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 52.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 2.3%; Score 53.4; DB 4; Length 1620;
Best Local Similarity 57.5%; Pred. No. 0.00025;

RESULT 782

ID AAS18543 standard; DNA; 18887 BP.

DE DNA encoding UDP glycosyltransferase 1 (UGT1A1).

PN WO200179230-A2.

PD 25-OCT-2001.

PA (GENA-) GENAISSANCE PHARM INC.

Query Match 2.3%; Score 53.4; DB 6; Length 18887;
Best Local Similarity 51.9%; Pred. No. 0.0013;

RESULT 783

ID AAA87255 standard; DNA; 223 BP.

DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:179.

PN WO200044902-A2.

PD 03-AUG-2000.

PA (SEAR) SEARLE & CO G D.

Query Match 2.3%; Score 53.2; DB 3; Length 223;
Best Local Similarity 63.9%; Pred. No. 7.7e-05;

RESULT 784

ID ABX43094 standard; cDNA; 393 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #8259.

PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 2.3%; Score 53.2; DB 8; Length 393;
 Best Local Similarity 50.5%; Pred. No. 0.00011;
 RESULT 785
 ID ABX36148 standard; cDNA; 383 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #1313.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 2.3%; Score 52.8; DB 8; Length 383;
 Best Local Similarity 52.2%; Pred. No. 0.00015;
 RESULT 786
 ID AAL61198 standard; DNA; 1209 BP.
 DE Actinosynnema pretiosum glycosyltransferase gene.
 PN WO2003045312-A2.
 PD 05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Query Match 2.3%; Score 52.6; DB 8; Length 1209;
 Best Local Similarity 62.6%; Pred. No. 0.00036;
 RESULT 787
 ID AAL61224 standard; DNA; 82746 BP.
 DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.
 PN WO2003045312-A2.
 PD 05-JUN-2003.
 PA (UNIW) UNIV WASHINGTON.
 Query Match 2.3%; Score 52.6; DB 8; Length 82746;
 Best Local Similarity 62.6%; Pred. No. 0.00059;
 RESULT 788
 ID ABV24713 standard; cDNA; 707 BP.
 DE Human prostate expression marker cDNA 24704.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.2%; Score 52; DB 5; Length 707;
 Best Local Similarity 54.2%; Pred. No. 0.00038;
 RESULT 789
 ID ADK56220 standard; DNA; 691 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #3603.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 Query Match 2.2%; Score 51; DB 10; Length 691;
 Best Local Similarity 60.4%; Pred. No. 0.00074;
 RESULT 790
 ID ADA69456 standard; DNA; 1494 BP.
 DE Rice gene, SEQ ID 2779.
 PN WO2003000898-A1.
 PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 2.2%; Score 50.4; DB 8; Length 1494;
 Best Local Similarity 61.4%; Pred. No. 0.0019;
 RESULT 791
 ID ADC25968 standard; cDNA; 1536 BP.
 DE Eucalyptus grandis UDP-glucosyltransferase cDNA.
 PN WO2003066836-A2.
 PD 14-AUG-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 2.2%; Score 50.4; DB 10; Length 1536;
 Best Local Similarity 57.7%; Pred. No. 0.0019;
 RESULT 792
 ID ADC25973 standard; cDNA; 1575 BP.
 DE Eucalyptus grandis UDP-glucosyltransferase cDNA variant.
 PN WO2003066836-A2.
 PD 14-AUG-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 2.2%; Score 50.4; DB 10; Length 1575;
 Best Local Similarity 57.7%; Pred. No. 0.0019;
 RESULT 793
 ID ABX78354 standard; cDNA; 1601 BP.
 DE Rice stress response protein cDNA.
 PN US2002152497-A1.
 PD 17-OCT-2002.
 PA (FALC/) FALCO S C.
 PA (FAMO/) FAMODU O O.
 PA (MEYE/) MEYERS B C.
 PA (MIAO/) MIAO G.
 PA (ODEL/) ODELL J T.
 PA (RAFA/) RAFALSKI J A.
 PA (THOR/) THORPE C J.
 PA (SAKA/) SAKAI H.
 PA (WENG/) WENG Z.
 Query Match 2.2%; Score 50.4; DB 10; Length 1601;
 Best Local Similarity 61.4%; Pred. No. 0.002;
 RESULT 794
 ID ADC08517 standard; DNA; 1999 BP.
 DE Rice DNA sequence Seq ID822 related to grain filling.
 PN WO2003000905-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 2.2%; Score 50.4; DB 10; Length 1999;
 Best Local Similarity 49.8%; Pred. No. 0.0023;
 RESULT 795
 ID ADF29092 standard; DNA; 131680 BP.
 DE Agrotis segetum granulovirus genomic DNA sequence, SEQ ID NO:1.
 PN CN1381581-A.
 PD 27-NOV-2002.
 PA (JIKA-) JIKANG BIOTECHNOLOGY CO LTD SHANGHAI.
 Query Match 2.2%; Score 50.4; DB 10; Length 131680;
 Best Local Similarity 48.1%; Pred. No. 0.037;
 RESULT 796
 ID ADJ11499 standard; DNA; 627 BP.
 DE Rice DNA modulated by post-transcriptional gene silencing SeqID 135.
 PN US2003135888-A1.
 PD 17-JUL-2003.
 PA (ZHUT/) ZHU T.

PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZE BROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.

Query Match 2.2%; Score 50.2; DB 11; Length 627;
Best Local Similarity 50.2%; Pred. No. 0.0012;

RESULT 797

ID ADP87526 standard; DNA; 1628 BP.
DE Japanese morning glory flavanone 3-hydroxylase DNA.
PN JP2004180592-A.
PD 02-JUL-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.

Query Match 2.1%; Score 49.8; DB 12; Length 1628;
Best Local Similarity 57.3%; Pred. No. 0.003;

RESULT 798

ID ABX78352 standard; cDNA; 398 BP.
DE Corn stress response protein EST #10.
PN US2002152497-A1.
PD 17-OCT-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.
PA (MIAO/) MIAO G.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (THOR/) THORPE C J.
PA (SAKA/) SAKAI H.
PA (WENG/) WENG Z.

Query Match 2.1%; Score 49.6; DB 10; Length 398;
Best Local Similarity 56.0%; Pred. No. 0.0014;

RESULT 799

ID ABV37264 standard; cDNA; 563 BP.
DE Human prostate expression marker cDNA 37255.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.1%; Score 49.6; DB 5; Length 563;
Best Local Similarity 54.8%; Pred. No. 0.0017;

RESULT 800

ID ABX78351 standard; cDNA; 932 BP.
DE Corn stress response protein EST #9.
PN US2002152497-A1.
PD 17-OCT-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (MEYE/) MEYERS B C.
PA (MIAO/) MIAO G.
PA (ODEL/) ODELL J T.
PA (RAFA/) RAFALSKI J A.
PA (THOR/) THORPE C J.

PA (SAKA/) SAKAI H.

PA (WENG/) WENG Z.

Query Match 2.1%; Score 49.6; DB 10; Length 932;

Best Local Similarity 56.0%; Pred. No. 0.0024;

RESULT 801

ID AAT62123 standard; cDNA to mRNA; 1578 BP.

DE Solanum melongena flavanoid-3-glucosyl transferase cDNA.

PN JP09056385-A.

PD 04-MAR-1997.

PA (KIRI) KIRIN BREWERY KK.

Query Match 2.1%; Score 49.4; DB 2; Length 1578;

Best Local Similarity 58.5%; Pred. No. 0.0039;

RESULT 802

ID AAH42961 standard; DNA; 656 BP.

DE Nucleic acid differentially expressed in Appl-d Drosophila.

PN WO200153538-A2.

PD 26-JUL-2001.

PA (NEUR-) NEUROSCIENCES RES FOUND INC.

Query Match 2.1%; Score 49.2; DB 4; Length 656;

Best Local Similarity 47.4%; Pred. No. 0.0025;

RESULT 803

ID ABX96761 standard; cDNA; 656 BP.

DE D. melanogaster differentially expressed mRNA EST GH04745.

PN US2002174447-A1.

PD 21-NOV-2002.

PA (GREE/) GREENSPAN R J.

PA (EDEL/) EDELMAN G M.

Query Match 2.1%; Score 49.2; DB 8; Length 656;

Best Local Similarity 47.4%; Pred. No. 0.0025;

RESULT 804

ID AAS05504 standard; DNA; 657 BP.

DE Mammalian vestibular system geotactic behaviour modulator gene #104.

PN WO200140519-A2.

PD 07-JUN-2001.

PA (NEUR-) NEUROSCIENCES RES FOUND INC.

Query Match 2.1%; Score 49.2; DB 5; Length 657;

Best Local Similarity 47.4%; Pred. No. 0.0025;

RESULT 805

ID ABL28715 standard; DNA; 1530 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37618.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 2.1%; Score 49.2; DB 4; Length 1530;

Best Local Similarity 59.2%; Pred. No. 0.0043;

RESULT 806

ID ABL20759 standard; DNA; 1752 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 13750.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 2.1%; Score 49.2; DB 4; Length 1752;

Best Local Similarity 47.4%; Pred. No. 0.0048;

RESULT 807

ID ABL28714 standard; DNA; 3679 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37615.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 2.1%; Score 49.2; DB 4; Length 3679;

Best Local Similarity 59.2%; Pred. No. 0.0078;

RESULT 808

ID ABV07329 standard; cDNA; 501 BP.

DE Human prostate expression marker cDNA 7320.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.1%; Score 49; DB 5; Length 501;

Best Local Similarity 54.8%; Pred. No. 0.0024;

RESULT 809

ID ADJ12032 standard; DNA; 1052 BP.

DE Wheat cDNA modulated by post-transcriptional gene silencing SeqID 668.

PN US2003135888-A1.

PD 17-JUL-2003.

PA (ZHUT/) ZHU T.

PA (WANG/) WANG X.

PA (CHAN/) CHANG H.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZE BROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.

PA (PROV/) PROVART N.

PA (RICK/) RICKE D.

Query Match 2.1%; Score 49; DB 11; Length 1052;

Best Local Similarity 57.5%; Pred. No. 0.0039;

RESULT 810

ID ABQ60746 standard; cDNA; 558 BP.

DE Human colon cancer related nucleotide sequence SEQ ID NO:4441.

PN WO200229086-A2.

PD 11-APR-2002.

PA (FARB) BAYER CORP.

Query Match 2.1%; Score 48.8; DB 6; Length 558;

Best Local Similarity 46.2%; Pred. No. 0.0029;

RESULT 811

ID ADA49280 standard; DNA; 666 BP.

DE Maize gene conferring disease resistance in plants.

PN WO2003000906-A2.

PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 2.1%; Score 48.6; DB 9; Length 666;

Best Local Similarity 58.7%; Pred. No. 0.0038;

RESULT 812

ID AAH51513 standard; DNA; 1001 BP.

DE Human UGT2B10 related DNA containing a biallelic polymorphism SEQ ID 404.

PN WO200058508-A2.

PD 05-OCT-2000.

PA (GEST) GENSET.

Query Match 2.1%; Score 48.6; DB 3; Length 1001;

Best Local Similarity 58.7%; Pred. No. 0.005;

RESULT 813

ID ADA71938 standard; DNA; 2000 BP.

DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 48.6; DB 8; Length 2000;
Best Local Similarity 12.4%; Pred. No. 0.0078;
RESULT 814
ID ADA49109 standard; DNA; 789 BP.
DE Wheat gene conferring disease resistance in plants.
PN WO2003000906-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 48.4; DB 9; Length 789;
Best Local Similarity 57.1%; Pred. No. 0.0049;
RESULT 815
ID ABZ12395 standard; DNA; 1437 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 200.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 48.4; DB 6; Length 1437;
Best Local Similarity 55.2%; Pred. No. 0.0072;
RESULT 816
ID ADA71206 standard; DNA; 1455 BP.
DE Rice gene, SEQ ID 4529.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 2.1%; Score 48.4; DB 8; Length 1455;
Best Local Similarity 58.2%; Pred. No. 0.0073;
RESULT 817
ID AAX60622 standard; DNA; 2396 BP.
DE M. brassicae ecdysteroid UDP-glucosyl transferase DNA.
PN JP11123079-A.
PD 11-MAY-1999.
PA (NOYA-) NOYAKU BIOTECHNOLOGY KAIHATSU.
Query Match 2.1%; Score 48.4; DB 2; Length 2396;
Best Local Similarity 55.3%; Pred. No. 0.01;
RESULT 818
ID ADJ11847 standard; DNA; 551 BP.
DE Banana cDNA modulated by post-transcriptional gene silencing SeqID 483.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZE BROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
Query Match 2.1%; Score 48.2; DB 11; Length 551;

Best Local Similarity 56.7%; Pred. No. 0.0044;
RESULT 819
ID ADJ43854 standard; cDNA; 551 BP.
DE Plant cDNA #4854.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.

Query Match 2.1%; Score 48.2; DB 12; Length 551;

Best Local Similarity 56.7%; Pred. No. 0.0044;

RESULT 820

ID ABX77212 standard; DNA; 75798 BP.
DE Mouse uridine diphosphoglucuronosyl transferase gene locus.
PN WO200283897-A1.
PD 24-OCT-2002.
PA (GENE-) GENE STREAM PTY LTD.

Query Match 2.1%; Score 48.2; DB 10; Length 75798;

Best Local Similarity 49.8%; Pred. No. 0.12;

RESULT 821

ID AAC39201 standard; DNA; 1689 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 23745.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 2.1%; Score 48; DB 3; Length 1689;

Best Local Similarity 56.2%; Pred. No. 0.011;

RESULT 822

ID ABK73606 standard; DNA; 1138 BP.
DE Bacillus licheniformis genomic sequence tag (GST) #897.
PN WO200229113-A2.
PD 11-APR-2002.
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.

Query Match 2.1%; Score 47.8; DB 6; Length 1138;

Best Local Similarity 51.7%; Pred. No. 0.0094;

RESULT 823

ID ADA69896 standard; DNA; 1410 BP.
DE Rice gene, SEQ ID 3219.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 2.0%; Score 47.4; DB 8; Length 1410;

Best Local Similarity 55.2%; Pred. No. 0.014;

RESULT 824

ID ADA11031 standard; cDNA; 334 BP.
DE Human cDNA differentially expressed in colon cancer #104.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE/) LASEK A W.

PA (JONE/) JONES D A.

Query Match 2.0%; Score 46.6; DB 9; Length 334;

Best Local Similarity 58.9%; Pred. No. 0.0095;

RESULT 825

ID AAD59156 standard; cDNA; 334 BP.

DE Human UDP-glucuronosyltransferase cDNA #1.

PN US2003073105-A1.

PD 17-APR-2003.

PA (LASE/) LASEK A K W.

PA (SORN/) SORNASSE T.

Query Match 2.0%; Score 46.6; DB 10; Length 334;

Best Local Similarity 58.9%; Pred. No. 0.0095;

RESULT 826

ID ADJ11840 standard; DNA; 634 BP.

DE Banana cDNA modulated by post-transcriptional gene silencing SeqID 476.

PN US2003135888-A1.

PD 17-JUL-2003.

PA (ZHUT/) ZHU T.

PA (WANG/) WANG X.

PA (CHAN/) CHANG H.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZE BROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.

PA (PROV/) PROVART N.

PA (RICK/) RICKE D.

Query Match 2.0%; Score 46.6; DB 11; Length 634;

Best Local Similarity 58.2%; Pred. No. 0.014;

RESULT 827

ID ABX40687 standard; cDNA; 315 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #5852.

PN US2002137139-A1.

PD 26-SEP-2002.

PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.

PA (WARR/) WARREN W C.

Query Match 2.0%; Score 46.4; DB 8; Length 315;

Best Local Similarity 50.0%; Pred. No. 0.01;

RESULT 828

ID ACC62594 standard; cDNA; 542 BP.

DE Rice endosperm EST #13.

PN CN1366079-A.

PD 28-AUG-2002.

PA (UYZH-) UNIV ZHEJIANG.

Query Match 2.0%; Score 46.4; DB 8; Length 542;

Best Local Similarity 55.6%; Pred. No. 0.015;

RESULT 829

ID AAD13658 standard; DNA; 1440 BP.

DE Arabidopsis thaliana glucosyltransferase (GTase) A42 gene.

PN WO200159140-A1.

PD 16-AUG-2001.

PA (UYYO-) UNIV YORK.

Query Match 2.0%; Score 46.4; DB 4; Length 1440;

Best Local Similarity 55.6%; Pred. No. 0.029;
 RESULT 830
 ID ABZ12275 standard; DNA; 1440 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 80.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 2.0%; Score 46.4; DB 6; Length 1440;
 Best Local Similarity 55.6%; Pred. No. 0.029;
 RESULT 831
 ID ADC25958 standard; DNA; 1440 BP.
 DE Thale cress UDP-glucosyltransferase DNA 2.
 PN WO2003066836-A2.
 PD 14-AUG-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 2.0%; Score 46.4; DB 10; Length 1440;
 Best Local Similarity 55.6%; Pred. No. 0.029;
 RESULT 832
 ID AAC47208 standard; DNA; 1688 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52959.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 2.0%; Score 46.4; DB 3; Length 1688;
 Best Local Similarity 55.6%; Pred. No. 0.032;
 RESULT 833
 ID ADL14332 standard; DNA; 1751 BP.
 DE DNA encoding a carnation glycosyltransferase enzyme SeqID 1.
 PN WO2004018682-A1.
 PD 04-MAR-2004.
 PA (SUNR) SUNTORY LTD.
 PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
 Query Match 2.0%; Score 46.4; DB 12; Length 1751;
 Best Local Similarity 51.4%; Pred. No. 0.033;
 RESULT 834
 ID AAL23790 standard; cDNA; 490 BP.
 DE Human breast cancer expressed polynucleotide 16247.
 PN WO200151628-A2.
 PD 19-JUL-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 2.0%; Score 46.2; DB 4; Length 490;
 Best Local Similarity 59.5%; Pred. No. 0.016;
 RESULT 835
 ID ADK59883 standard; DNA; 631 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #7266.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 Query Match 2.0%; Score 46.2; DB 10; Length 631;
 Best Local Similarity 55.2%; Pred. No. 0.019;
 RESULT 836
 ID ADA70992 standard; DNA; 1458 BP.
 DE Rice gene, SEQ ID 4315.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 2.0%; Score 46.2; DB 8; Length 1458;
 Best Local Similarity 57.1%; Pred. No. 0.033;
 RESULT 837
 ID ADA70251 standard; DNA; 1464 BP.
 DE Rice gene, SEQ ID 3574.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 2.0%; Score 46.2; DB 8; Length 1464;
 Best Local Similarity 57.1%; Pred. No. 0.033;
 RESULT 838
 ID ABX34472 standard; cDNA; 1983 BP.
 DE Human mddt cDNA SEQ ID 33.
 PN WO200279449-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 2.0%; Score 46.2; DB 8; Length 1983;
 Best Local Similarity 53.6%; Pred. No. 0.041;
 RESULT 839
 ID ABL17597 standard; DNA; 1477 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4264.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.0%; Score 46; DB 4; Length 1477;
 Best Local Similarity 44.7%; Pred. No. 0.038;
 RESULT 840
 ID ABL17596 standard; DNA; 3528 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4261.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 2.0%; Score 46; DB 4; Length 3528;
 Best Local Similarity 44.7%; Pred. No. 0.068;
 RESULT 841
 ID ADA71335 standard; DNA; 1395 BP.
 DE Rice gene, SEQ ID 4658.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 2.0%; Score 45.8; DB 8; Length 1395;
 Best Local Similarity 57.2%; Pred. No. 0.042;
 RESULT 842
 ID ABL32281 standard; DNA; 13511 BP.
 DE Human immune system associated gene SEQ ID NO: 254.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 2.0%; Score 45.8; DB 6; Length 13511;
 Best Local Similarity 50.7%; Pred. No. 0.19;
 RESULT 843
 ID ABL34609 standard; DNA; 18585 BP.
 DE Human metastasis associated gene SEQ ID NO: 162.
 PN WO200177376-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 2.0%; Score 45.8; DB 6; Length 18585;

Best Local Similarity 49.4%; Pred. No. 0.24;
 RESULT 844
 ID ADS99870 standard; DNA; 18585 BP.
 DE Complement of bisulphite treated metastasis-associated human gene #81.
 PN US2003148327-A1.
 PD 07-AUG-2003.
 PA (OLEK/) OLEK A.
 PA (PIEP/) PIEPENBROCK C.
 PA (BERL/) BERLIN K.
 Query Match 2.0%; Score 45.8; DB 7; Length 18585;
 Best Local Similarity 49.4%; Pred. No. 0.24;
 RESULT 845
 ID ADS65831 standard; cDNA; 242 BP.
 DE Corn seedling-derived polynucleotide (cpds), SEQ ID 847.
 PN US2003237110-A9.
 PD 25-DEC-2003.
 PA (INCY-) INCYTE PHARM INC.
 Query Match 1.9%; Score 45.2; DB 7; Length 242;
 Best Local Similarity 59.2%; Pred. No. 0.02;
 RESULT 846
 ID ADA69839 standard; DNA; 1383 BP.
 DE Rice gene, SEQ ID 3162.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.9%; Score 45.2; DB 8; Length 1383;
 Best Local Similarity 55.8%; Pred. No. 0.064;
 RESULT 847
 ID ADA70476 standard; DNA; 1452 BP.
 DE Rice gene, SEQ ID 3799.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.9%; Score 45.2; DB 8; Length 1452;
 Best Local Similarity 55.8%; Pred. No. 0.066;
 RESULT 848
 ID ADA48529 standard; DNA; 1549 BP.
 DE Rice gene conferring disease resistance in plants.
 PN WO2003000906-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.9%; Score 45.2; DB 9; Length 1549;
 Best Local Similarity 55.8%; Pred. No. 0.069;
 RESULT 849
 ID ABX78358 standard; cDNA; 1736 BP.
 DE Wheat stress response protein cDNA #2.
 PN US2002152497-A1.
 PD 17-OCT-2002.
 PA (FALC/) FALCO S C.
 PA (FAMO/) FAMODU O O.
 PA (MEYE/) MEYERS B C.
 PA (MIAO/) MIAO G.
 PA (ODEL/) ODELL J T.
 PA (RAFA/) RAFALSKI J A.
 PA (THOR/) THORPE C J.
 PA (SAKA/) SAKAI H.
 PA (WENG/) WENG Z.

Query Match 1.9%; Score 45.2; DB 10; Length 1736;
 Best Local Similarity 55.8%; Pred. No. 0.074;

RESULT 850
 ID ADA72551 standard; DNA; 2000 BP.
 DE Rice gene, SEQ ID 5876.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.9%; Score 45.2; DB 8; Length 2000;
 Best Local Similarity 55.8%; Pred. No. 0.081;

RESULT 851
 ID AAC58024 standard; DNA; 45 BP.
 DE Human PRO1780 hybridisation probe SEQ ID NO:16.
 PN WO200053750-A1.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 3; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 852
 ID AAA37270 standard; DNA; 45 BP.
 DE Human PRO1780 hybridisation probe SEQ ID NO:285.
 PN WO200012708-A2.
 PD 09-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 3; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 853
 ID AAF54404 standard; DNA; 45 BP.
 DE Primer #83 used in the identification of proteins.
 PN WO200078961-A1.
 PD 28-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 4; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 854
 ID ACD68443 standard; DNA; 45 BP.
 DE Novel human secreted and transmembrane protein related probe #41.
 PN US2003073130-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 9; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 855
 ID ACH04545 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003044841-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 9; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 856
 ID ACD68089 standard; DNA; 45 BP.
 DE Novel human secreted and transmembrane protein related probe #41.
 PN US2003073129-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 9; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 857
 ID ADC18154 standard; DNA; 45 BP.
 DE Human PRO probe #41.
 PN US2003064925-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 858
 ID ADD70800 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003099625-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 859
 ID ADD39877 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003083462-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 860
 ID ADD70323 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003054406-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 861
 ID ADD38444 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003096955-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 862
 ID ADD39400 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003096954-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 863
 ID ADD38923 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003092061-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 864

ID ADD40354 standard; DNA; 45 BP.

DE Human secreted/transmembrane protein PRO1780 probe.

PN US2003082627-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 865

ID ADE50575 standard; DNA; 45 BP.

DE Human secreted/transmembrane protein PRO1780 probe.

PN US2003069179-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 866

ID ADE20187 standard; DNA; 45 BP.

DE Human secreted/transmembrane protein PRO1780 probe.

PN US2003092883-A1.

PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 867

ID ADE50098 standard; DNA; 45 BP.

DE Human secreted/transmembrane protein PRO1780 probe.

PN US2003082626-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 868

ID ADE21656 standard; DNA; 45 BP.

DE Human secreted/transmembrane protein PRO1780 probe.

PN US2003082628-A1.

PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 869

ID ADF30081 standard; DNA; 45 BP.

DE Human secreted/transmembrane protein PRO1780 probe.

PN US2003204053-A1.

PD 30-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 870

ID ADF55974 standard; DNA; 45 BP.

DE Human secreted/transmembrane protein PRO1780 probe.

PN US2003204054-A1.

PD 30-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 1.9%; Score 45; DB 10; Length 45;

Best Local Similarity 100.0%; Pred. No. 0.0075;

RESULT 871

ID ADH99478 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003065142-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 872
 ID ADE96658 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003195347-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 873
 ID ADF25969 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003199675-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 874
 ID ADF24868 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003198993-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 875
 ID ADF29604 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003203401-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 876
 ID ADE97135 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003195334-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 877
 ID ADH03173 standard; DNA; 45 BP.
 DE Human secreted/transmembrane protein PRO1780 probe.
 PN US2003216562-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.9%; Score 45; DB 12; Length 45;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 RESULT 878
 ID ADH04127 standard; DNA; 45 BP.

DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003220471-A1..
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 879
ID ADH03650 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 880
ID ADH04604 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 881
ID ADH61605 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 882
ID ADL94804 standard; DNA; 45 BP.
DE Human secreted/transmembrane protein PRO1780 probe.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 1.9%; Score 45; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0075;
RESULT 883
ID ADC25977 standard; DNA; 1515 BP.
DE Calamondin plant UDP-glucosyltransferase DNA.
PN WO2003066836-A2.
PD 14-AUG-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.9%; Score 45; DB 10; Length 1515;
Best Local Similarity 56.4%; Pred. No. 0.078; --
RESULT 884
ID AAI71192 standard; cDNA; 1536 BP.
DE Citrus unshiu UDP-D glucose:limonoid glucosyltransferase cDNA SEQ:10.
PN JP2001204477-A.
PD 31-JUL-2001.
PA (NORQ) NORINSUISANSHO KAJU SHIKENBACHO.
Query Match 1.9%; Score 45; DB 4; Length 1536;
Best Local Similarity 56.4%; Pred. No. 0.078;
RESULT 885
ID ADC25980 standard; DNA; 1560 BP.
DE Calamondin plant UDP-glucosyltransferase DNA variant.

PN WO2003066836-A2.
 PD 14-AUG-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.9%; Score 45; DB 10; Length 1560;
 Best Local Similarity 56.4%; Pred. No. 0.079;
 RESULT 886
 ID AAI71187 standard; cDNA; 1732 BP.
 DE Citrus unshiu UDP-D glucose:limonoid glucosyltransferase cDNA SEQ:1.
 PN JP2001204477-A.
 PD 31-JUL-2001.
 PA (NORQ) NORINSUISANSHO KAJU SHIKENBACHO.
 Query Match 1.9%; Score 45; DB 4; Length 1732;
 Best Local Similarity 56.4%; Pred. No. 0.085;
 RESULT 887
 ID AAI96011 standard; cDNA; 774 BP.
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2086.
 PN WO200166719-A1.
 PD 13-SEP-2001.
 PA (CHIB-) CHIBA PREFECTURE.
 PA (HISM) HISAMITSU PHARM CO LTD.
 Query Match 1.9%; Score 44.8; DB 4; Length 774;
 Best Local Similarity 55.9%; Pred. No. 0.057;
 RESULT 888
 ID AAC43085 standard; DNA; 1362 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37972.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.9%; Score 44.8; DB 3; Length 1362;
 Best Local Similarity 55.0%; Pred. No. 0.083;
 RESULT 889
 ID ABZ14612 standard; DNA; 1362 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2417.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.9%; Score 44.8; DB 6; Length 1362;
 Best Local Similarity 55.0%; Pred. No. 0.083;
 RESULT 890
 ID ADG87939 standard; cDNA; 1362 BP.
 DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #381.
 PN WO200222675-A2.
 PD 21-MAR-2002.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA (UYNC-) UNIV NORTH CAROLINA.
 PA (GLAZ/) GLAZEBROOK J.
 PA (WANG/) WANG X.
 PA (DANG/) DANGL J L.
 PA (EULG/) EULGEM T.
 PA (ZHUT/) ZHU T.
 Query Match 1.9%; Score 44.8; DB 6; Length 1362;
 Best Local Similarity 55.0%; Pred. No. 0.083;
 RESULT 891
 ID ABZ42019 standard; cDNA; 1362 BP.
 DE Arabidopsis thaliana gene #3 modulated by PTGS.
 PN WO200281695-A2.
 PD 17-OCT-2002.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (FRIE-) FRIEDRICH MIESCHER INST.
Query Match 1.9%; Score 44.8; DB 8; Length 1362;
Best Local Similarity 55.0%; Pred. No. 0.083;
RESULT 892
ID ADA68251 standard; DNA; 1362 BP.
DE Arabidopsis thaliana gene, SEQ ID 899.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 44.8; DB 8; Length 1362;
Best Local Similarity 55.0%; Pred. No. 0.083;
RESULT 893
ID AAA68125 standard; DNA; 762 BP.
DE Pinus radiata flavonol glucosyl transferase DNA sequence SEQ ID NO:218.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 1.9%; Score 44.6; DB 3; Length 762;
Best Local Similarity 57.6%; Pred. No. 0.065;
RESULT 894
ID ADD41875 standard; DNA; 762 BP.
DE Flavonol glucosyl transferase DNA.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 1.9%; Score 44.6; DB 10; Length 762;
Best Local Similarity 57.6%; Pred. No. 0.065;
RESULT 895
ID ADC25964 standard; cDNA; 1437 BP.
DE Grape UDP-glucosyltransferase cDNA.
PN WO2003066836-A2.
PD 14-AUG-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.9%; Score 44.6; DB 10; Length 1437;
Best Local Similarity 55.5%; Pred. No. 0.099;
RESULT 896
ID AAT68693 standard; cDNA; 432 BP.
DE Strawberry UDP-glucuronosyl transferase cDNA.
PN WO9721816-A1.
PD 19-JUN-1997.
PA (ZENE) ZENECA LTD.
Query Match 1.9%; Score 43.8; DB 2; Length 432;
Best Local Similarity 56.6%; Pred. No. 0.077;
RESULT 897
ID ADA70053 standard; DNA; 1152 BP.
DE Rice gene, SEQ ID 3376.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.9%; Score 43.8; DB 8; Length 1152;
Best Local Similarity 56.6%; Pred. No. 0.15;
RESULT 898
ID ADJ11565 standard; DNA; 1152 BP.
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 201.

PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZE BROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.

Query Match 1.9%; Score 43.8; DB 11; Length 1152;
Best Local Similarity 56.6%; Pred. No. 0.15;

RESULT 899

ID ADA69724 standard; DNA; 1482 BP.
DE Rice gene, SEQ ID 3047.
PN WO2003000898-A1.
PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.9%; Score 43.8; DB 8; Length 1482;
Best Local Similarity 54.7%; Pred. No. 0.17;

RESULT 900

ID AAI61373 standard; DNA; 513445 BP.
DE Soybean 318013 region A3, SEQ ID NO: 4.
PN WO200151627-A2.
PD 19-JUL-2001.
PA (MONS) MONSANTO CO.

Query Match 1.9%; Score 43.8; DB 5; Length 110000;
Best Local Similarity 53.1%; Pred. No. 3;

RESULT 901

ID AAH51524 standard; DNA; 1001 BP.
DE Human UGT2B15 related DNA containing a biallelic polymorphism SEQ ID 415.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.

Query Match 1.9%; Score 43.6; DB 3; Length 1001;
Best Local Similarity 56.2%; Pred. No. 0.15;

RESULT 902

ID AAH51522 standard; DNA; 1001 BP.
DE Human UGT2B15 related DNA containing a biallelic polymorphism SEQ ID 413.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.

Query Match 1.9%; Score 43.6; DB 3; Length 1001;
Best Local Similarity 56.2%; Pred. No. 0.15;

RESULT 903

ID AAH51523 standard; DNA; 1001 BP.
DE Human UGT2B15 related DNA containing a biallelic polymorphism SEQ ID 414.
PN WO200058508-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.

Query Match 1.9%; Score 43.6; DB 3; Length 1001;
Best Local Similarity 56.2%; Pred. No. 0.15;

RESULT 904

ID AAH51526 standard; DNA; 1001 BP.
 DE Human UGT2B15 related DNA containing a biallelic polymorphism SEQ ID 417.
 PN WO200058508-A2.
 PD 05-OCT-2000.
 PA (GEST) GENSET.
 Query Match 1.9%; Score 43.6; DB 3; Length 1001;
 Best Local Similarity 56.2%; Pred. No. 0.15;
 RESULT 905
 ID AAZ95208 standard; DNA; 1020 BP.
 DE Human UGT2B15 exon 2 nucleotide sequence.
 PN WO200006776-A1.
 PD 10-FEB-2000.
 PA (AXYS-) AXYS PHARM INC.
 Query Match 1.9%; Score 43.6; DB 3; Length 1020;
 Best Local Similarity 56.2%; Pred. No. 0.16;
 RESULT 906
 ID ABZ13997 standard; DNA; 1350 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1802.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.9%; Score 43.6; DB 6; Length 1350;
 Best Local Similarity 56.2%; Pred. No. 0.19;
 RESULT 907
 ID ADG87992 standard; cDNA; 1350 BP.
 DE A. thaliana RPP4-upregulated pathogen infection-related gene #434.
 PN WO200222675-A2.
 PD 21-MAR-2002.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA (UYN-) UNIV NORTH CAROLINA.
 PA (GLAZ/) GLAZEBROOK J.
 PA (WANG/) WANG X.
 PA (DANG/) DANGL J L.
 PA (EULG/) EULGEM T.
 PA (ZHUT/) ZHU T.
 Query Match 1.9%; Score 43.6; DB 6; Length 1350;
 Best Local Similarity 56.2%; Pred. No. 0.19;
 RESULT 908
 ID ADA68085 standard; DNA; 1350 BP.
 DE Arabidopsis thaliana gene, SEQ ID 345.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.9%; Score 43.6; DB 8; Length 1350;
 Best Local Similarity 56.2%; Pred. No. 0.19;
 RESULT 909
 ID AAD13679 standard; DNA; 1437 BP.
 DE Arabidopsis thaliana glucosyltransferase (GTase) UGT74F2 DNA.
 PN WO200159140-A1.
 PD 16-AUG-2001.
 PA (UYYO-) UNIV YORK.
 Query Match 1.9%; Score 43.6; DB 4; Length 1437;
 Best Local Similarity 56.2%; Pred. No. 0.2;
 RESULT 910
 ID ADJ83915 standard; DNA; 1437 BP.
 DE Thale cress glucosyltransferase 74F2 ORF DNA.

PN WO2003106688-A1.
 PD 24-DEC-2003.
 PA (UYYO-) UNIV YORK.
 Query Match 1.9%; Score 43.6; DB 12; Length 1437;
 Best Local Similarity 56.2%; Pred. No. 0.2;
 RESULT 911
 ID AAC42649 standard; DNA; 1527 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36344.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.9%; Score 43.6; DB 3; Length 1527;
 Best Local Similarity 56.2%; Pred. No. 0.2;
 RESULT 912
 ID AAC37656 standard; DNA; 1565 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 18186.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.9%; Score 43.6; DB 3; Length 1565;
 Best Local Similarity 53.5%; Pred. No. 0.21;
 RESULT 913
 ID ADJ44409 standard; cDNA; 678 BP.
 DE Plant cDNA #5409.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZE BROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 PA (ZHUT/) ZHU T.
 Query Match 1.9%; Score 43.4; DB 12; Length 678;
 Best Local Similarity 56.7%; Pred. No. 0.14;
 RESULT 914
 ID ADA71177 standard; DNA; 1359 BP.
 DE Rice gene, SEQ ID 4500.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.9%; Score 43.4; DB 8; Length 1359;
 Best Local Similarity 54.1%; Pred. No. 0.22;
 RESULT 915
 ID AAH51525 standard; DNA; 1001 BP.
 DE Human UGT2B15 related DNA containing a biallelic polymorphism SEQ ID 416.
 PN WO200058508-A2.
 PD 05-OCT-2000.
 PA (GEST) GENSET.
 Query Match 1.9%; Score 43.2; DB 3; Length 1001;
 Best Local Similarity 55.5%; Pred. No. 0.2;
 RESULT 916
 ID ABL34122 standard; DNA; 10329 BP.
 DE Human immune system associated gene SEQ ID NO: 2095.
 PN WO200200928-A2.

PD 03-JAN-2002.

PA . (EPIG-) EPIGENOMICS AG.

Query Match 1.9%; Score 43.2; DB 6; Length 10329;

Best Local Similarity 50.0%; Pred. No. 0.96;

RESULT 917

ID ADA49272 standard; DNA; 393 BP.

DE Maize gene conferring disease resistance in plants.

PN WO2003000906-A2.

PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.9%; Score 43; DB 9; Length 393;

Best Local Similarity 54.0%; Pred. No. 0.13;

RESULT 918

ID ADJ44737 standard; cDNA; 393 BP.

DE Plant cDNA #5737.

PN US2004016025-A1.

PD 22-JAN-2004.

PA (BUDW/) BUDWORTH P.

PA (MOUG/) MOUGHAMER T.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZE BROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (PROV/) PROVART N.

PA (RICK/) RICKE D.

PA (ZHUT/) ZHU T.

Query Match 1.9%; Score 43; DB 12; Length 393;

Best Local Similarity 54.0%; Pred. No. 0.13;

RESULT 919

ID ADJ83914 standard; DNA; 1350 BP.

DE Thale cress glucosyltransferase 74F1 ORF DNA.

PN WO2003106688-A1.

PD 24-DEC-2003.

PA (UYYO-) UNIV YORK.

Query Match 1.9%; Score 43; DB 12; Length 1350;

Best Local Similarity 56.8%; Pred. No. 0.28;

RESULT 920

ID AAA54024 standard; DNA; 1440 BP.

DE Glucosyltransferase coding sequence.

PN WO200055340-A1.

PD 21-SEP-2000.

PA (PION-) PIONEER HI-BRED INT INC.

Query Match 1.9%; Score 43; DB 3; Length 1440;

Best Local Similarity 52.5%; Pred. No. 0.3;

RESULT 921

ID ADK59884 standard; DNA; 557 BP.

DE Plant DNA sequence which confers altered metabolic characteristic #7267.

PN WO2003020936-A1.

PD 13-MAR-2003.

PA (DOWC) DOW CHEM CO.

PA (DOWC) DOW AGROSCIENCES LLC.

Query Match 1.8%; Score 42.8; DB 10; Length 557;

Best Local Similarity 55.3%; Pred. No. 0.18;

RESULT 922

ID ADA70052 standard; DNA; 1476 BP.

DE Rice gene, SEQ ID 3375.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.8%; Score 42.8; DB 8; Length 1476;
 Best Local Similarity 55.3%; Pred. No. 0.35;
 RESULT 923
 ID AAA87154 standard; DNA; 164 BP.
 DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:78.
 PN WO200044902-A2.
 PD 03-AUG-2000.
 PA (SEAR) SEARLE & CO G D.
 Query Match 1.8%; Score 42.6; DB 3; Length 164;
 Best Local Similarity 68.7%; Pred. No. 0.092;
 RESULT 924
 ID ACC49462 standard; cDNA; 1368 BP.
 DE Arabidopsis glucosyltransferase 75B2 nucleic acid sequence.
 PN WO2003023035-A2.
 PD 20-MAR-2003.
 PA (UYYO-) UNIV YORK.
 Query Match 1.8%; Score 42.6; DB 8; Length 1368;
 Best Local Similarity 51.3%; Pred. No. 0.38;
 RESULT 925
 ID AAV29492 standard; cDNA to mRNA; 2025 BP.
 DE DNA encoding ecdysteroid UDP-glycosyl transferase.
 PN WO9814578-A1.
 PD 09-APR-1998.
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (AMCY) AMERICAN CYANAMID CO.
 Query Match 1.8%; Score 42.6; DB 2; Length 2025;
 Best Local Similarity 51.9%; Pred. No. 0.49;
 RESULT 926
 ID AAD07242 standard; DNA; 2025 BP.
 DE HzSNPV ecdysteroid UDP-glucosyltransferase (egt) gene.
 PN US6235278-B1.
 PD 22-MAY-2001.
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (AMCY) AMERICAN CYANAMID CO.
 Query Match 1.8%; Score 42.6; DB 5; Length 2025;
 Best Local Similarity 51.9%; Pred. No. 0.49;
 RESULT 927
 ID ABA81171 standard; DNA; 121 BP.
 DE UGT1 mutation correcting oligonucleotide SEQ ID NO: 4017.
 PN WO200173002-A2.
 PD 04-OCT-2001.
 PA (UYDE) UNIV DELAWARE.
 Query Match 1.8%; Score 42.4; DB 4; Length 121;
 Best Local Similarity 60.3%; Pred. No. 0.087;
 RESULT 928
 ID ABA81170 standard; DNA; 121 BP.
 DE UGT1 mutation correcting oligonucleotide SEQ ID NO: 4016.
 PN WO200173002-A2.
 PD 04-OCT-2001.
 PA (UYDE) UNIV DELAWARE.
 Query Match 1.8%; Score 42.4; DB 4; Length 121;
 Best Local Similarity 60.3%; Pred. No. 0.087;
 RESULT 929

ID ABX47099 standard; cDNA; 234 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #12264.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 1.8%; Score 42.4; DB 8; Length 234;
 Best Local Similarity 57.6%; Pred. No. 0.13;
 RESULT 930
 ID ADK56213 standard; DNA; 372 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #3596.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 Query Match 1.8%; Score 42.4; DB 10; Length 372;
 Best Local Similarity 56.4%; Pred. No. 0.18;
 RESULT 931
 ID AAD13655 standard; DNA; 1410 BP.
 DE Arabidopsis thaliana glucosyltransferase (GTase) A062 gene.
 PN WO200159140-A1.
 PD 16-AUG-2001.
 PA (UYYO-) UNIV YORK.
 Query Match 1.8%; Score 42.4; DB 4; Length 1410;
 Best Local Similarity 51.6%; Pred. No. 0.44;
 RESULT 932
 ID ACC49461 standard; cDNA; 1410 BP.
 DE Arabidopsis glucosyltransferase 75B1 nucleic acid sequence.
 PN WO2003023035-A2.
 PD 20-MAR-2003.
 PA (UYYO-) UNIV YORK.
 Query Match 1.8%; Score 42.4; DB 8; Length 1410;
 Best Local Similarity 51.6%; Pred. No. 0.44;
 RESULT 933
 ID ABZ80609 standard; DNA; 1410 BP.
 DE Arabidopsis thaliana glucosyltransferase clone 75B1.
 PN WO2002103022-A2.
 PD 27-DEC-2002.
 PA (UYYO-) UNIV YORK.
 Query Match 1.8%; Score 42.4; DB 8; Length 1410;
 Best Local Similarity 51.6%; Pred. No. 0.44;
 RESULT 934
 ID ABZ14576 standard; DNA; 1428 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2381.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.8%; Score 42.4; DB 6; Length 1428;
 Best Local Similarity 52.2%; Pred. No. 0.45;
 RESULT 935
 ID ADC25962 standard; DNA; 1428 BP.
 DE Thale cress UDP-glucosyltransferase DNA 3.
 PN WO2003066836-A2.
 PD 14-AUG-2003.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.8%; Score 42.4; DB 10; Length 1428;
 Best Local Similarity 52.2%; Pred. No. 0.45;

RESULT 936
 ID AAD13659 standard; DNA; 1430 BP.
 DE Arabidopsis thaliana glucosyltransferase (GTase) A43 gene.
 PN WO200159140-A1.
 PD 16-AUG-2001.
 PA (UYYO-) UNIV YORK.
 Query Match 1.8%; Score 42.4; DB 4; Length 1430;
 Best Local Similarity 52.2%; Pred. No. 0.45;

RESULT 937
 ID AAC47235 standard; DNA; 1533 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53061.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.8%; Score 42.4; DB 3; Length 1533;
 Best Local Similarity 52.2%; Pred. No. 0.47;

RESULT 938
 ID AAC43061 standard; DNA; 1560 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37881.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.8%; Score 42.4; DB 3; Length 1560;
 Best Local Similarity 51.6%; Pred. No. 0.47;

RESULT 939
 ID ADG88168 standard; cDNA; 1560 BP.
 DE A. thaliana RPP4-upregulated pathogen infection-related gene #610.
 PN WO200222675-A2.
 PD 21-MAR-2002.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA (UYNC-) UNIV NORTH CAROLINA.
 PA (GLAZ/) GLAZE BROOK J.
 PA (WANG/) WANG X.
 PA (DANG/) DANG J L.
 PA (EULG/) EULGEM T.
 PA (ZHUT/) ZHU T.
 Query Match 1.8%; Score 42.4; DB 6; Length 1560;
 Best Local Similarity 51.6%; Pred. No. 0.47;

RESULT 940
 ID ADA70893 standard; DNA; 1563 BP.
 DE Rice gene, SEQ ID 4216.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.8%; Score 42.4; DB 8; Length 1563;
 Best Local Similarity 55.4%; Pred. No. 0.47;

RESULT 941
 ID AAC50249 standard; DNA; 1779 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 64128.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.8%; Score 42.4; DB 3; Length 1779;
 Best Local Similarity 51.6%; Pred. No. 0.52;

RESULT 942
 ID ADA71938 standard; DNA; 2000 BP.
 DE Rice gene, SEQ ID 5263.

PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.8%; Score 42.4; DB 8; Length 2000;
 Best Local Similarity 8.7%; Pred. No. 0.56;
 RESULT 943
 Query Match 1.8%; Score 42.4; DB 5; Length 110000;
 Best Local Similarity 52.9%; Pred. No. 8;
 RESULT 944
 ID ABN85750 standard; DNA; 180557 BP.
 DE Human BAC clone RP11-334G22 SEQ ID NO 6.
 PN US2002119929-A1.
 PD 29-AUG-2002.
 PA (BISH/) BISHOP C E.
 PA (AGOU/) AGOULNIK A I.
 PA (ZHUQ/) ZHU Q.
 Query Match 1.8%; Score 42.4; DB 6; Length 180557;
 Best Local Similarity 48.0%; Pred. No. 11;
 RESULT 945
 ID ABL34073 standard; DNA; 40862 BP.
 DE Human immune system associated gene SEQ ID NO: 2046.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.8%; Score 42.2; DB 6; Length 40862;
 Best Local Similarity 49.8%; Pred. No. 4.7;
 RESULT 946
 ID AAC40101 standard; DNA; 1525 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27052.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.8%; Score 42; DB 3; Length 1525;
 Best Local Similarity 51.7%; Pred. No. 0.61;
 RESULT 947
 ID AAQ10336 standard; DNA; 1800 BP.
 DE Ecdysteroid UDP-glucosyl transferase gene.
 PN WO9100014-A.
 PD 10-JAN-1991.
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 Query Match 1.8%; Score 42; DB 2; Length 1800;
 Best Local Similarity 51.0%; Pred. No. 0.68;
 RESULT 948
 ID AAT17233 standard; DNA; 2793 BP.
 DE AcMNPV L-1 egt gene region.
 PN WO9603509-A2.
 PD 08-FEB-1996.
 PA (AMCY) AMERICAN CYANAMID CO.
 Query Match 1.8%; Score 42; DB 2; Length 2793;
 Best Local Similarity 51.0%; Pred. No. 0.92;
 RESULT 949
 ID AAF23741 standard; DNA; 2793 BP.
 DE egt coding sequence.
 PN US6156309-A.
 PD 05-DEC-2000.
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA (AMCY) AMERICAN CYANAMID CO.

Query Match 1.8%; Score 42; DB 4; Length 2793;
 Best Local Similarity 51.0%; Pred. No. 0.92;
 RESULT 950
 ID ABQ67150 standard; DNA; 40324 BP.
 DE Human angiogenesis associated polynucleotide SEQ ID NO 180.
 PN WO200246454-A2.
 PD 13-JUN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.8%; Score 42; DB 6; Length 40324;
 Best Local Similarity 47.1%; Pred. No. 5.4;
 RESULT 951
 ID ADC51644 standard; DNA; 50000 BP.
 DE BmNPV genomic DNA nucleotides 1-50000.
 PN JP2003024062-A.
 PD 28-JAN-2003.
 PA (RIKA) RIKAGAKU KENKYUSHO.
 Query Match 1.8%; Score 42; DB 10; Length 50000;
 Best Local Similarity 51.0%; Pred. No. 6.2;
 RESULT 952
 ID AAT13635 standard; DNA; 133894 BP.
 DE AcNPV genomic DNA clone 6.
 PN WO9601320-A2.
 PD 18-JAN-1996.
 PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
 Query Match 1.8%; Score 42; DB 2; Length 133894;
 Best Local Similarity 51.0%; Pred. No. 12;
 RESULT 953
 ID ADN98817 standard; cDNA; 957 BP.
 DE Novel human cDNA sequence #417.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 1.8%; Score 41.8; DB 12; Length 957;
 Best Local Similarity 50.2%; Pred. No. 0.52;
 RESULT 954
 ID ADO00386 standard; cDNA; 957 BP.
 DE Novel human cDNA sequence #1201.
 PN WO2004038003-A2.
 PD 06-MAY-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 1.8%; Score 41.8; DB 12; Length 957;
 Best Local Similarity 50.2%; Pred. No. 0.52;
 RESULT 955
 ID ADN97656 standard; DNA; 1218 BP.
 DE S ambofaciens spiramycin biosynthetic gene ORF26.
 PN WO2004033689-A2.
 PD 22-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS.
 Query Match 1.8%; Score 41.8; DB 12; Length 1218;
 Best Local Similarity 50.8%; Pred. No. 0.61;
 RESULT 956
 ID AAC51291 standard; DNA; 1470 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 67973.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.8%; Score 41.8; DB 3; Length 1470;

Best Local Similarity 57.1%; Pred. No. 0.69;
 RESULT 957
 ID ADN73090 standard; cDNA; 1470 BP.
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 985.
 PN WO2004035798-A2.
 PD 29-APR-2004.
 PA (CROP-) CROPDESIGN NV.
 Query Match 1.8%; Score 41.8; DB 12; Length 1470;
 Best Local Similarity 57.1%; Pred. No. 0.69;
 RESULT 958
 ID AAX02828 standard; cDNA; 2062 BP.
 DE WO9905287 Seq ID 3.
 PN WO9905287-A1.
 PD 04-FEB-1999.
 PA (SUNR) SUNTORY LTD.
 Query Match 1.8%; Score 41.8; DB 2; Length 2062;
 Best Local Similarity 50.2%; Pred. No. 0.86;
 RESULT 959
 ID ADN97683 standard; DNA; 6174 BP.
 DE S ambofaciens spiramycin biosynthetic gene related sequence.
 PN WO2004033689-A2.
 PD 22-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS.
 Query Match 1.8%; Score 41.8; DB 12; Length 6174;
 Best Local Similarity 50.8%; Pred. No. 1.8;
 RESULT 960
 ID ADN97655 standard; DNA; 10325 BP.
 DE S ambofaciens spiramycin biosynthetic gene related sequence.
 PN WO2004033689-A2.
 PD 22-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS.
 Query Match 1.8%; Score 41.8; DB 12; Length 10325;
 Best Local Similarity 50.8%; Pred. No. 2.5;
 RESULT 961
 ID ADN97689 standard; DNA; 12134 BP.
 DE S ambofaciens spiramycin biosynthetic gene related sequence.
 PN WO2004033689-A2.
 PD 22-APR-2004.
 PA (AVET) AVENTIS PHARMA SA.
 PA (CNRS) CNRS.
 Query Match 1.8%; Score 41.8; DB 12; Length 12134;
 Best Local Similarity 50.8%; Pred. No. 2.8;
 RESULT 962
 ID ADA70300 standard; DNA; 1323 BP.
 DE Rice gene, SEQ ID 3623.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.8%; Score 41.6; DB 8; Length 1323;
 Best Local Similarity 55.6%; Pred. No. 0.73;
 RESULT 963
 ID ABL32448 standard; DNA; 7238 BP.
 DE Human immune system associated gene SEQ ID NO: 421.
 PN WO200200928-A2.
 PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.8%; Score 41.6; DB 6; Length 7238;
 Best Local Similarity 49.5%; Pred. No. 2.3;

RESULT 964
 ID AAD13683 standard; DNA; 1434 BP.
 DE Arabidopsis thaliana glucosyltransferase (GTase) UGT76E2 DNA.
 PN WO200159140-A1.
 PD 16-AUG-2001.
 PA (UYYO-) UNIV YORK.
 Query Match 1.8%; Score 41.4; DB 4; Length 1434;
 Best Local Similarity 53.4%; Pred. No. 0.89;

RESULT 965
 ID AAC36320 standard; DNA; 1507 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 13360.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.8%; Score 41.4; DB 3; Length 1507;
 Best Local Similarity 53.4%; Pred. No. 0.92;

RESULT 966
 ID ABZ13771 standard; DNA; 1374 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1576.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.8%; Score 41.2; DB 6; Length 1374;
 Best Local Similarity 55.6%; Pred. No. 0.99;

RESULT 967
 ID ADA68399 standard; DNA; 1374 BP.
 DE Arabidopsis thaliana gene, SEQ ID 718.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.8%; Score 41.2; DB 8; Length 1374;
 Best Local Similarity 55.6%; Pred. No. 0.99;

RESULT 968
 ID ADN73930 standard; cDNA; 1374 BP.
 DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 1825.
 PN WO2004035798-A2.
 PD 29-APR-2004.
 PA (CROP-) CROPDESIGN NV.
 Query Match 1.8%; Score 41.2; DB 12; Length 1374;
 Best Local Similarity 55.6%; Pred. No. 0.99;

RESULT 969
 ID ADA71282 standard; DNA; 4686 BP.
 DE Rice gene, SEQ ID 4605.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.8%; Score 41.2; DB 8; Length 4686;
 Best Local Similarity 57.9%; Pred. No. 2.2;

RESULT 970
 ID ABL33105 standard; DNA; 7829 BP.
 DE Human immune system associated gene SEQ ID NO: 1078.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.

Query Match 1.8%; Score 41.2; DB 6; Length 7829;
 Best Local Similarity 49.5%; Pred. No. 3.1;
 RESULT 971
 ID ABK31287 standard; DNA; 7829 BP.
 DE Signal transduction associated gene modified complementary DNA #65.
 PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.8%; Score 41.2; DB 6; Length 7829;
 Best Local Similarity 49.5%; Pred. No. 3.1;
 RESULT 972
 ID ABL70266 standard; DNA; 7829 BP.
 DE Chemically treated cell signalling DNA sequence complementary to #78.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.8%; Score 41.2; DB 6; Length 7829;
 Best Local Similarity 49.5%; Pred. No. 3.1;
 RESULT 973
 ID AAS61191 standard; DNA; 7829 BP.
 DE Human gene regulation-associated gene oligonucleotide #146.
 PN WO200177375-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.8%; Score 41.2; DB 6; Length 7829;
 Best Local Similarity 49.5%; Pred. No. 3.1;
 RESULT 974
 ID ABL32893 standard; DNA; 10710 BP.
 DE Human immune system associated gene SEQ ID NO: 866.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.8%; Score 41.2; DB 6; Length 10710;
 Best Local Similarity 49.5%; Pred. No. 3.9;
 RESULT 975
 ID ADJ39974 standard; cDNA; 485 BP.
 DE Plant cDNA #974.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZE BROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 PA (ZHUT/) ZHU T.
 Query Match 1.8%; Score 41; DB 12; Length 485;
 Best Local Similarity 55.2%; Pred. No. 0.57;
 RESULT 976
 ID ADA70477 standard; DNA; 1479 BP.
 DE Rice gene, SEQ ID 3800.
 PN WO2003000898-A1.
 PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 41; DB 8; Length 1479;
Best Local Similarity 55.2%; Pred. No. 1.2;
RESULT 977
ID ADA72552 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5877.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 41; DB 8; Length 2000;
Best Local Similarity 55.2%; Pred. No. 1.5;
RESULT 978
ID ACN45034 standard; DNA; 99588 BP.
DE Human genomic sequence hCG1640838.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.8%; Score 41; DB 11; Length 99588;
Best Local Similarity 50.8%; Pred. No. 20;
RESULT 979
ID AAA87085 standard; DNA; 366 BP.
DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:6.
PN WO200044902-A2.
PD 03-AUG-2000.
PA (SEAR) SEARLE & CO G D.
Query Match 1.8%; Score 40.8; DB 3; Length 366;
Best Local Similarity 50.8%; Pred. No. 0.54;
RESULT 980
ID ACN57109 standard; cDNA; 623 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-014-Q6-K6-D3, SEQ:11890.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 1.8%; Score 40.8; DB 13; Length 623;
Best Local Similarity 55.7%; Pred. No. 0.77;
RESULT 981
ID ADA69887 standard; DNA; 1398 BP.
DE Rice gene, SEQ ID 3210.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.8%; Score 40.8; DB 8; Length 1398;
Best Local Similarity 55.7%; Pred. No. 1.3;
RESULT 982
Query Match 1.8%; Score 40.8; DB 6; Length 110000;
Best Local Similarity 50.0%; Pred. No. 24;
RESULT 983
Query Match 1.8%; Score 40.8; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 24;
RESULT 984
Query Match 1.8%; Score 40.8; DB 12; Length 110000;
Best Local Similarity 50.0%; Pred. No. 24;
RESULT 985
Query Match 1.8%; Score 40.8; DB 12; Length 110000;

Best Local Similarity 50.0%; Pred. No. 24;

RESULT 986

ID ABX43759 standard; cDNA; 427 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #8924.

PN US2002137139-A1.

PD 26-SEP-2002.

PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.

PA (WARR/) WARREN W C.

Query Match 1.7%; Score 40.4; DB 8; Length 427;

Best Local Similarity 50.0%; Pred. No. 0.79;

RESULT 987

ID ADA69472 standard; DNA; 1437 BP.

DE Rice gene, SEQ ID 2795.

PN WO2003000898-A1.

PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.7%; Score 40.4; DB 8; Length 1437;

Best Local Similarity 54.8%; Pred. No. 1.8;

RESULT 988

ID ACC49459 standard; cDNA; 1440 BP.

DE Arabidopsis glucosyltransferase 71B6 nucleic acid sequence.

PN WO2003023035-A2.

PD 20-MAR-2003.

PA (UYYO-) UNIV YORK.

Query Match 1.7%; Score 40.4; DB 8; Length 1440;

Best Local Similarity 52.3%; Pred. No. 1.8;

RESULT 989

ID ADJ11934 standard; DNA; 468 BP.

DE Wheat cDNA modulated by post-transcriptional gene silencing SeqID 570.

PN US2003135888-A1.

PD 17-JUL-2003.

PA (ZHUT/) ZHU T.

PA (WANG/) WANG X.

PA (CHAN/) CHANG H.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.

PA (PROV/) PROVART N.

PA (RICK/) RICKE D.

Query Match 1.7%; Score 40.2; DB 11; Length 468;

Best Local Similarity 55.3%; Pred. No. 0.96;

RESULT 990

ID ADN74714 standard; cDNA; 1383 BP.

DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2609.

PN WO2004035798-A2.

PD 29-APR-2004.

PA (CROP-) CROPDESIGN NV.

Query Match 1.7%; Score 40.2; DB 12; Length 1383;

Best Local Similarity 54.4%; Pred. No. 2;

RESULT 991

ID ADR70667 standard; cDNA; 1613 BP.

DE Solanum aculeatisimum glycosylase encoding cDNA SEQ ID NO:4.
PN WO2004078979-A1.
PD 16-SEP-2004.
PA (RIKE) RIKEN KK.
Query Match 1.7%; Score 40.2; DB 13; Length 1613;
Best Local Similarity 50.8%; Pred. No. 2.2;
RESULT 992
ID ADR70665 standard; cDNA; 1673 BP.
DE Solanum aculeatisimum glycosylase encoding cDNA SEQ ID NO:2.
PN WO2004078979-A1.
PD 16-SEP-2004.
PA (RIKE) RIKEN KK.
Query Match 1.7%; Score 40.2; DB 13; Length 1673;
Best Local Similarity 50.8%; Pred. No. 2.2;
RESULT 993
ID ADA70478 standard; DNA; 1350 BP.
DE Rice gene, SEQ ID 3801.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.7%; Score 40; DB 8; Length 1350;
Best Local Similarity 53.2%; Pred. No. 2.2;
RESULT 994
ID AAC51614 standard; DNA; 1362 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69162.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 1.7%; Score 40; DB 3; Length 1362;
Best Local Similarity 53.9%; Pred. No. 2.2;
RESULT 995
ID AAD13682 standard; DNA; 1457 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) UGT76E12 DNA.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.
Query Match 1.7%; Score 40; DB 4; Length 1457;
Best Local Similarity 53.9%; Pred. No. 2.4;
RESULT 996
ID ABL33993 standard; DNA; 6029 BP.
DE Human immune system associated gene SEQ ID NO: 1966.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 40; DB 6; Length 6029;
Best Local Similarity 49.1%; Pred. No. 6;
RESULT 997
ID ABL32860 standard; DNA; 7631 BP.
DE Human immune system associated gene SEQ ID NO: 833.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.7%; Score 40; DB 6; Length 7631;
Best Local Similarity 53.9%; Pred. No. 7.1;
RESULT 998
ID ABL34228 standard; DNA; 8576 BP.
DE Human immune system associated gene SEQ ID NO: 2201.
PN WO200200928-A2.

PD 03-JAN-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 1.7%; Score 40; DB 6; Length 8576;
 Best Local Similarity 49.1%; Pred. No. 7.6;
 RESULT 999
 ID ABL33418 standard; DNA; 10716 BP.
 DE Human immune system associated gene SEQ ID NO: 1391.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 1.7%; Score 40; DB 6; Length 10716;
 Best Local Similarity 49.1%; Pred. No. 8.8;
 RESULT 1000
 ID ABL33414 standard; DNA; 17389 BP.
 DE Human immune system associated gene SEQ ID NO: 1387.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 1.7%; Score 40; DB 6; Length 17389;
 Best Local Similarity 47.5%; Pred. No. 12;
 RESULT 1001
 ID ABL70604 standard; DNA; 34548 BP.
 DE Chemically treated cell signalling DNA sequence complementary to#247.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 1.7%; Score 40; DB 6; Length 34548;
 Best Local Similarity 49.1%; Pred. No. 19;
 RESULT 1002
 ID ABZ84585 standard; cDNA; 433 BP.
 DE Toxicologically relevant human nucleotide sequence #1744.
 PN WO2003016500-A2.
 PD 27-FEB-2003.
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 Query Match 1.7%; Score 39.8; DB 10; Length 433;
 Best Local Similarity 47.0%; Pred. No. 1.2;
 RESULT 1003
 ID ABZ13712 standard; DNA; 1371 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1517.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.7%; Score 39.8; DB 6; Length 1371;
 Best Local Similarity 52.8%; Pred. No. 2.6;
 RESULT 1004
 ID ADG88170 standard; cDNA; 1371 BP.
 DE A. thaliana RPP4-upregulated pathogen infection-related gene #612.
 PN WO200222675-A2.
 PD 21-MAR-2002.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA (UYNC-) UNIV NORTH CAROLINA.
 PA (GLAZ/) GLAZEBROOK J.
 PA (WANG/) WANG X.
 PA (DANG/) DANGL J L.
 PA (EULG/) EULGEM T.
 PA (ZHUT/) ZHU T.

Query Match 1.7%; Score 39.8; DB 6; Length 1371;
 Best Local Similarity 52.8%; Pred. No. 2.6;
 RESULT 1005
 ID ACC49463 standard; cDNA; 1371 BP.
 DE Arabidopsis glucosyltransferase 84B1 nucleic acid sequence.
 PN WO2003023035-A2.
 PD 20-MAR-2003.
 PA (UYYO-) UNIV YORK.
 Query Match 1.7%; Score 39.8; DB 8; Length 1371;
 Best Local Similarity 53.5%; Pred. No. 2.6;
 RESULT 1006
 ID ADA69788 standard; DNA; 1407 BP.
 DE Rice gene, SEQ ID 3111.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.7%; Score 39.8; DB 8; Length 1407;
 Best Local Similarity 52.0%; Pred. No. 2.6;
 RESULT 1007
 ID ADJ40077 standard; cDNA; 1407 BP.
 DE Plant cDNA #1077.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZEBROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 PA (ZHUT/) ZHU T.
 Query Match 1.7%; Score 39.8; DB 12; Length 1407;
 Best Local Similarity 52.0%; Pred. No. 2.6;
 RESULT 1008
 ID AAD13660 standard; DNA; 1437 BP.
 DE Arabidopsis thaliana glucosyltransferase (GTase) A911 gene.
 PN WO200159140-A1.
 PD 16-AUG-2001.
 PA (UYYO-) UNIV YORK.
 Query Match 1.7%; Score 39.8; DB 4; Length 1437;
 Best Local Similarity 53.5%; Pred. No. 2.7;
 RESULT 1009
 ID AAD13680 standard; DNA; 1451 BP.
 DE Arabidopsis thaliana glucosyltransferase (GTase) UGT76E1 DNA.
 PN WO200159140-A1.
 PD 16-AUG-2001.
 PA (UYYO-) UNIV YORK.
 Query Match 1.7%; Score 39.8; DB 4; Length 1451;
 Best Local Similarity 52.8%; Pred. No. 2.7;
 RESULT 1010
 ID AAD13686 standard; DNA; 1494 BP.
 DE Arabidopsis thaliana glucosyltransferase (GTase) UGT72B3 DNA.
 PN WO200159140-A1.
 PD 16-AUG-2001.

PA (UYYO-) UNIV YORK.

Query Match 1.7%; Score 39.8; DB 4; Length 1494;

Best Local Similarity 56.5%; Pred. No. 2.7;

RESULT 1011

ID AAC50671 standard; DNA; 1505 BP.

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 65708.

PN EP1033405-A2.

PD 06-SEP-2000.

Query Match 1.7%; Score 39.8; DB 3; Length 1505;

Best Local Similarity 52.8%; Pred. No. 2.8;

RESULT 1012

ID ACC49460 standard; cDNA; 2559 BP.

DE Arabidopsis glucosyltransferase 74D1 nucleic acid sequence.

PN WO2003023035-A2.

PD 20-MAR-2003.

PA (UYYO-) UNIV YORK.

Query Match 1.7%; Score 39.8; DB 8; Length 2559;

Best Local Similarity 52.8%; Pred. No. 3.9;

RESULT 1013

ID AAA87491 standard; DNA; 273 BP.

DE Rat hepatocyte carcinogenesis biomarker nucleic acid SEQ ID NO:415.

PN WO200044902-A2.

PD 03-AUG-2000.

PA (SEAR) SEARLE & CO G D.

Query Match 1.7%; Score 39.6; DB 3; Length 273;

Best Local Similarity 48.8%; Pred. No. 1;

RESULT 1014

ID ADA69807 standard; DNA; 1419 BP.

DE Rice gene, SEQ ID 3130.

PN WO2003000898-A1.

PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.7%; Score 39.6; DB 8; Length 1419;

Best Local Similarity 54.0%; Pred. No. 3;

RESULT 1015

ID AAD13681 standard; DNA; 1433 BP.

DE Arabidopsis thaliana glucosyltransferase (GTase) UGT76E11 DNA.

PN WO200159140-A1.

PD 16-AUG-2001.

PA (UYYO-) UNIV YORK.

Query Match 1.7%; Score 39.6; DB 4; Length 1433;

Best Local Similarity 54.9%; Pred. No. 3.1;

RESULT 1016

ID AAC51615 standard; DNA; 1594 BP.

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69166.

PN EP1033405-A2.

PD 06-SEP-2000.

Query Match 1.7%; Score 39.6; DB 3; Length 1594;

Best Local Similarity 54.9%; Pred. No. 3.3;

RESULT 1017

ID AAC39330 standard; DNA; 1596 BP.

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24233.

PN EP1033405-A2.

PD 06-SEP-2000.

Query Match 1.7%; Score 39.6; DB 3; Length 1596;

Best Local Similarity 54.9%; Pred. No. 3.3;

RESULT 1018

ID AAD55726 standard; DNA; 5858 BP.
 DE Nephila madagascariensis major ampullate spidroin 2 (MaSp2)-like DNA.
 PN WO2003020916-A2.
 PD 13-MAR-2003.
 PA (UYWY-) UNIV WYOMING.
 Query Match 1.7%; Score 39.6; DB 8; Length 5858;
 Best Local Similarity 46.9%; Pred. No. 7.8;
 RESULT 1019
 ID ABL33367 standard; DNA; 6104 BP.
 DE Human immune system associated gene SEQ ID NO: 1340.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.7%; Score 39.6; DB 6; Length 6104;
 Best Local Similarity 47.6%; Pred. No. 8;
 RESULT 1020
 ID ABL12934 standard; cDNA; 8004 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 33284.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.7%; Score 39.6; DB 4; Length 8004;
 Best Local Similarity 45.5%; Pred. No. 9.6;
 RESULT 1021
 ID ABL12928 standard; cDNA; 8736 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 33266.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.7%; Score 39.6; DB 4; Length 8736;
 Best Local Similarity 45.5%; Pred. No. 10;
 RESULT 1022
 ID AAS27804 standard; DNA; 31168 BP.
 DE DNA encoding novel signal transduction pathway protein, Seq ID 1464.
 PN WO200154733-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.7%; Score 39.6; DB 4; Length 31168;
 Best Local Similarity 56.0%; Pred. No. 24;
 RESULT 1023
 ID ABA07295 standard; DNA; 31168 BP.
 DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 614.
 PN WO200155206-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.7%; Score 39.6; DB 4; Length 31168;
 Best Local Similarity 56.0%; Pred. No. 24;
 RESULT 1024
 ID AAS42115 standard; DNA; 31168 BP.
 DE Genomic sequence #431 encoding novel human enzyme polypeptide.
 PN WO200155301-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.7%; Score 39.6; DB 4; Length 31168;
 Best Local Similarity 56.0%; Pred. No. 24;
 RESULT 1025
 ID AAK89940 standard; DNA; 31168 BP.

DE Human digestive system antigen genomic sequence SEQ ID NO: 3516.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.7%; Score 39.6; DB 4; Length 31168;
 Best Local Similarity 56.0%; Pred. No. 24;
 RESULT 1026
 ID AAK64760 standard; DNA; 31168 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19572.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.7%; Score 39.6; DB 4; Length 31168;
 Best Local Similarity 56.0%; Pred. No. 24;
 RESULT 1027
 ID ADB94607 standard; DNA; 31168 BP.
 DE Novel human protein DNA #216.
 PN US2002168711-A1.
 PD 14-NOV-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 1.7%; Score 39.6; DB 10; Length 31168;
 Best Local Similarity 56.0%; Pred. No. 24;
 RESULT 1028
 ID AAA09469 standard; DNA; 50937 BP.
 DE Streptococcus oleandomycin gene cluster.
 PN WO200026349-A2.
 PD 11-MAY-2000.
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 Query Match 1.7%; Score 39.6; DB 3; Length 50937;
 Best Local Similarity 52.4%; Pred. No. 33;
 RESULT 1029
 Query Match 1.7%; Score 39.6; DB 8; Length 110000;
 Best Local Similarity 61.8%; Pred. No. 55;
 RESULT 1030
 ID ADA68696 standard; DNA; 640 BP.
 DE Rice gene, SEQ ID 2019.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.7%; Score 39.4; DB 8; Length 640;
 Best Local Similarity 55.5%; Pred. No. 2.1;
 RESULT 1031
 ID AAD13666 standard; DNA; 1437 BP.
 DE Arabidopsis thaliana glucosyltransferase (GTase) UGT71B5. DNA.
 PN WO200159140-A1.
 PD 16-AUG-2001.
 PA (UYYO-) UNIV YORK.
 Query Match 1.7%; Score 39.4; DB 4; Length 1437;
 Best Local Similarity 52.8%; Pred. No. 3.5;
 RESULT 1032
 ID ADA68496 standard; DNA; 1437 BP.
 DE Arabidopsis thaliana gene, SEQ ID 612.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.7%; Score 39.4; DB 8; Length 1437;
 Best Local Similarity 52.8%; Pred. No. 3.5;
 RESULT 1033
 ID ABL05597 standard; cDNA; 1921 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 11273.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.7%; Score 39.4; DB 4; Length 1921;
 Best Local Similarity 45.6%; Pred. No. 4.3;
 RESULT 1034
 ID ADL14347 standard; DNA; 1993 BP.
 DE DNA encoding a carnation glycosyltransferase enzyme SeqID 16.
 PN WO2004018682-A1.
 PD 04-MAR-2004.
 PA (SUNR) SUNTORY LTD.
 PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
 Query Match 1.7%; Score 39.4; DB 12; Length 1993;
 Best Local Similarity 52.8%; Pred. No. 4.4;
 RESULT 1035
 ID ABL05596 standard; cDNA; 4141 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 11270.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.7%; Score 39.4; DB 4; Length 4141;
 Best Local Similarity 45.6%; Pred. No. 7.1;
 RESULT 1036
 ID ABN80023 standard; DNA; 6636 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 40.
 PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.7%; Score 39.4; DB 6; Length 6636;
 Best Local Similarity 46.8%; Pred. No. 9.7;
 RESULT 1037
 ID ABL32605 standard; DNA; 11155 BP.
 DE Human immune system associated gene SEQ ID NO: 578.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.7%; Score 39.4; DB 6; Length 11155;
 Best Local Similarity 51.5%; Pred. No. 14;
 RESULT 1038
 ID ABK31511 standard; DNA; 47108 BP.
 DE Signal transduction associated gene modified complementary DNA #177.
 PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.7%; Score 39.4; DB 6; Length 47108;
 Best Local Similarity 48.4%; Pred. No. 36;
 RESULT 1039
 ID AAF65250 standard; cDNA; 378 BP.
 DE Novel human polynucleotide, SEQ ID NO: 1006.
 PN WO200102568-A2.
 PD 11-JAN-2001.
 PA (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.

Query Match 1.7%; Score 39.2; DB 5; Length 378;

Best Local Similarity 58.6%; Pred. No. 1.7;

RESULT 1040

ID ADM65498 standard; DNA; 482 BP.

DE NRY polymorphism detection primer #438.

PN US2003134285-A1.

PD 17-JUL-2003.

PA (OEFN/) OEFNER P J.

PA (UNDE/) UNDERHILL P A.

Query Match 1.7%; Score 39.2; DB 11; Length 482;

Best Local Similarity 55.0%; Pred. No. 2;

RESULT 1041

ID AAH53768 standard; DNA; 486 BP.

DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:2929.

PN WO200134809-A2.

PD 17-MAY-2001.

PA (GLAX) GLAXO GROUP LTD.

Query Match 1.7%; Score 39.2; DB 4; Length 486;

Best Local Similarity 55.0%; Pred. No. 2;

RESULT 1042

ID ABN91345 standard; DNA; 492 BP.

DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:808.

PN US6380370-B1.

PD 30-APR-2002.

PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 1.7%; Score 39.2; DB 6; Length 492;

Best Local Similarity 55.0%; Pred. No. 2;

RESULT 1043

ID AAF08725 standard; cDNA; 578 BP.

DE Fusarium venenatum EST SEQ ID NO:1248.

PN WO200056762-A2.

PD 28-SEP-2000.

PA (NOVO) NOVO NORDISK BIOTECH INC.

PA (NOVO) NOVO NORDISK AS.

Query Match 1.7%; Score 39.2; DB 3; Length 578;

Best Local Similarity 47.7%; Pred. No. 2.2;

RESULT 1044

ID ADJ12024 standard; DNA; 661 BP.

DE Wheat cDNA modulated by post-transcriptional gene silencing SeqID 660.

PN US2003135888-A1.

PD 17-JUL-2003.

PA (ZHUT/) ZHU T.

PA (WANG/) WANG X.

PA (CHAN/) CHANG H.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZE BROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.

PA (PROV/) PROVART N.

PA (RICK/) RICKE D.

Query Match 1.7%; Score 39.2; DB 11; Length 661;

Best Local Similarity 55.0%; Pred. No. 2.4;

RESULT 1045

ID AAC53614 standard; DNA; 1676 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 75115.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.7%; Score 39.2; DB 3; Length 1676;
 Best Local Similarity 51.7%; Pred. No. 4.5;
 RESULT 1046
 ID AAC54823 standard; DNA; 1676 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 79218.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.7%; Score 39.2; DB 3; Length 1676;
 Best Local Similarity 51.7%; Pred. No. 4.5;
 RESULT 1047
 ID AAH54132 standard; DNA; 3994 BP.
 DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3496.
 PN WO200134809-A2.
 PD 17-MAY-2001.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match 1.7%; Score 39.2; DB 4; Length 3994;
 Best Local Similarity 55.0%; Pred. No. 8;
 RESULT 1048
 ID ADJ43498 standard; cDNA; 503 BP.
 DE Plant cDNA #4498.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZE BROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 PA (ZHUT/) ZHU T.
 Query Match 1.7%; Score 39; DB 12; Length 503;
 Best Local Similarity 55.6%; Pred. No. 2.3;
 RESULT 1049
 ID AAZ45117 standard; DNA; 759 BP.
 DE UDP-glucuronosyltransferase 1 (UGT1) exon 1J nucleotide sequence.
 PN WO9957322-A2.
 PD 11-NOV-1999.
 PA (AXYS-) AXYS PHARM INC.
 Query Match 1.7%; Score 39; DB 3; Length 759;
 Best Local Similarity 52.8%; Pred. No. 3;
 RESULT 1050
 ID AAZ45116 standard; DNA; 930 BP.
 DE UDP-glucuronosyltransferase 1 (UGT1) exon 1H nucleotide sequence.
 PN WO9957322-A2.
 PD 11-NOV-1999.
 PA (AXYS-) AXYS PHARM INC.
 Query Match 1.7%; Score 39; DB 3; Length 930;
 Best Local Similarity 52.8%; Pred. No. 3.5;
 RESULT 1051
 ID AAQ13726 standard; DNA; 1200 BP.

DE Zeaxanthin glycosylase - engineered.
 PN WO9113078-A.
 PD 05-SEP-1991.
 PA (STAD) AMOCO CORP.
 Query Match 1.7%; Score 39; DB 2; Length 1200;
 Best Local Similarity 63.2%; Pred. No. 4.1;
 RESULT 1052
 ID AAD30176 standard; DNA; 1244 BP.
 DE Human UDP-glucuronosyl transferase (UGT1A8) gene exon 1.
 PN WO200206523-A2.
 PD 24-JAN-2002.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Query Match 1.7%; Score 39; DB 6; Length 1244;
 Best Local Similarity 52.8%; Pred. No. 4.2;
 RESULT 1053
 ID AAD30175 standard; DNA; 1452 BP.
 DE Human UDP-glucuronosyl transferase (UGT1A10) gene exon 1.
 PN WO200206523-A2.
 PD 24-JAN-2002.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Query Match 1.7%; Score 39; DB 6; Length 1452;
 Best Local Similarity 52.8%; Pred. No. 4.7;
 RESULT 1054
 ID ABL33154 standard; DNA; 5807 BP.
 DE Human immune system associated gene SEQ ID NO: 1127.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.7%; Score 39; DB 6; Length 5807;
 Best Local Similarity 48.8%; Pred. No. 12;
 RESULT 1055
 ID ABL33972 standard; DNA; 7771 BP.
 DE Human immune system associated gene SEQ ID NO: 1945.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.7%; Score 39; DB 6; Length 7771;
 Best Local Similarity 48.8%; Pred. No. 14;
 RESULT 1056
 ID ADM98599 standard; DNA; 12753 BP.
 DE Geranylgeranyl pyrophosphate synthase DNA #19.
 PN US2004072323-A1.
 PD 15-APR-2004.
 PA (MATS/) MATSUDA S P T.
 PA (HART/) HART E A.
 Query Match 1.7%; Score 39; DB 12; Length 12753;
 Best Local Similarity 63.2%; Pred. No. 20;
 RESULT 1057
 ID ABA58871 standard; DNA; 478 BP.
 DE Human foetal liver single exon nucleic acid probe #7176.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 1.7%; Score 38.8; DB 4; Length 478;
 Best Local Similarity 47.2%; Pred. No. 2.6;
 RESULT 1058
 ID AAI38585 standard; DNA; 478 BP.

DE Probe #7271 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 4; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1059
ID AAK32772 standard; DNA; 478 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 7329.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 4; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1060
ID AAK07031 standard; DNA; 478 BP.
DE Human brain expressed single exon probe SEQ ID NO: 7022.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 4; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1061
ID ABS32491 standard; DNA; 478 BP.
DE Human liver single exon probe, SEQ ID No 7481.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 4; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1062
ID ABS07570 standard; DNA; 478 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 7561.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 1.7%; Score 38.8; DB 6; Length 478;
Best Local Similarity 47.2%; Pred. No. 2.6;
RESULT 1063
ID ADM65495 standard; DNA; 482 BP.
DE NRY polymorphism detection primer #436.
PN US2003134285-A1.
PD 17-JUL-2003.
PA (OEFN/) OEFNER P J.
PA (UNDE/) UNDERHILL P A.
Query Match 1.7%; Score 38.8; DB 11; Length 482;
Best Local Similarity 54.3%; Pred. No. 2.6;
RESULT 1064
ID ADJ12104 standard; DNA; 1134 BP.
DE Maize cDNA modulated by post-transcriptional gene silencing SeqID 740.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHUT/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.

PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.

Query Match 1.7%; Score 38.8; DB 11; Length 1134;
Best Local Similarity 52.5%; Pred. No. 4.5;

RESULT 1065

ID ADJ44631 standard; cDNA; 1134 BP.
DE Plant cDNA #5631.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.

Query Match 1.7%; Score 38.8; DB 12; Length 1134;
Best Local Similarity 52.5%; Pred. No. 4.5;

RESULT 1066

ID ABL32539 standard; DNA; 5820 BP.
DE Human immune system associated gene SEQ ID NO: 512.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.7%; Score 38.8; DB 6; Length 5820;
Best Local Similarity 49.2%; Pred. No. 13;

RESULT 1067

ID ABL33758 standard; DNA; 7455 BP.
DE Human immune system associated gene SEQ ID NO: 1731.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.7%; Score 38.8; DB 6; Length 7455;
Best Local Similarity 46.9%; Pred. No. 16;

RESULT 1068

ID ABL32669 standard; DNA; 11049 BP.
DE Human immune system associated gene SEQ ID NO: 642.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.7%; Score 38.8; DB 6; Length 11049;
Best Local Similarity 54.1%; Pred. No. 21;

RESULT 1069

ID ABL92219 standard; DNA; 11049 BP.
DE Chemically treated DNA repair gene fragment complementary to#14.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.7%; Score 38.8; DB 6; Length 11049;
 Best Local Similarity 54.1%; Pred. No. 21;
 RESULT 1070
 ID ABL49322 standard; DNA; 11049 BP.
 DE Human polynucleotide associated with DNA replication SEQ ID NO 22.
 PN WO200177377-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.7%; Score 38.8; DB 6; Length 11049;
 Best Local Similarity 54.1%; Pred. No. 21;
 RESULT 1071
 ID ABL33900 standard; DNA; 11662 BP.
 DE Human immune system associated gene SEQ ID NO: 1873.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.7%; Score 38.8; DB 6; Length 11662;
 Best Local Similarity 48.2%; Pred. No. 21;
 RESULT 1072
 ID ADQ97617 standard; DNA; 57008 BP.
 DE Human cancer associated sequence HD10-015, SEQ ID 594.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.7%; Score 38.8; DB 12; Length 57008;
 Best Local Similarity 67.1%; Pred. No. 61;
 RESULT 1073
 ID ADK56217 standard; DNA; 640 BP.
 DE Plant DNA sequence which confers altered metabolic characteristic #3600.
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 Query Match 1.7%; Score 38.6; DB 10; Length 640;
 Best Local Similarity 53.7%; Pred. No. 3.6;
 RESULT 1074
 ID ADC25996 standard; DNA; 1494 BP.
 DE Oilseed rape UDP-glucosyltransferase DNA.
 PN WO2003066836-A2.
 PD 14-AUG-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.7%; Score 38.6; DB 10; Length 1494;
 Best Local Similarity 53.7%; Pred. No. 6.3;
 RESULT 1075
 ID AAA70223 standard; DNA; 3549 BP.
 DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:356.
 PN WO200025728-A2.
 PD 11-MAY-2000.
 PA (HOFF/) HOFFMAN S.
 PA (CARU/) CARUCCI D.
 PA (GARD/) GARDNER M.
 PA (VENT/) VENTER J C.
 Query Match 1.7%; Score 38.6; DB 3; Length 3549;
 Best Local Similarity 48.0%; Pred. No. 11;
 RESULT 1076
 ID ABN80086 standard; DNA; 7922 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 103.

PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.7%; Score 38.6; DB 6; Length 7922;
 Best Local Similarity 50.3%; Pred. No. 19;
 RESULT 1077
 ID ADA47985 standard; DNA; 912 BP.
 DE Rice gene conferring disease resistance in plants.
 PN WO2003000906-A2.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.7%; Score 38.4; DB 9; Length 912;
 Best Local Similarity 55.1%; Pred. No. 5.2;
 RESULT 1078
 ID AAQ33027 standard; DNA; 1667 BP.
 DE Exon 5 from the UGT1 gene locus.
 PN WO9212987-A1.
 PD 06-AUG-1992.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 Query Match 1.7%; Score 38.4; DB 2; Length 1667;
 Best Local Similarity 48.2%; Pred. No. 7.7;
 RESULT 1079
 ID ABL02054 standard; cDNA; 4652 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 644.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.7%; Score 38.4; DB 4; Length 4652;
 Best Local Similarity 52.5%; Pred. No. 15;
 RESULT 1080
 ID ABK28348 standard; DNA; 6076 BP.
 DE DNA transcription associated complementary genomic DNA #111.
 PN WO200192565-A2.
 PD 06-DEC-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.7%; Score 38.4; DB 6; Length 6076;
 Best Local Similarity 52.5%; Pred. No. 18;
 RESULT 1081
 ID AAA68075 standard; DNA; 330 BP.
 DE Pinus radiata CGT nucleotide sequence SEQ ID NO:168.
 PN WO200022099-A1.
 PD 20-APR-2000.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 Query Match 1.6%; Score 38.2; DB 3; Length 330;
 Best Local Similarity 55.7%; Pred. No. 3;
 RESULT 1082
 ID ADD41825 standard; DNA; 330 BP.
 DE Coniferol glucosyl transferase DNA #9.
 PN US2003131373-A1.
 PD 10-JUL-2003.
 PA (BLOK/) BLOKSBERG L N.
 PA (HAVU/) HAVUKKALA I.
 Query Match 1.6%; Score 38.2; DB 10; Length 330;
 Best Local Similarity 55.7%; Pred. No. 3;
 RESULT 1083
 ID ADN74274 standard; cDNA; 1263 BP.

DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2169.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 1.6%; Score 38.2; DB 12; Length 1263;
Best Local Similarity 50.3%; Pred. No. 7.4;
RESULT 1084
ID ADA69637 standard; DNA; 1460 BP.
DE Rice gene, SEQ ID 2960.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.6%; Score 38.2; DB 8; Length 1460;
Best Local Similarity 46.4%; Pred. No. 8.1;
RESULT 1085
ID ABL03434 standard; cDNA; 3633 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4784.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 38.2; DB 4; Length 3633;
Best Local Similarity 50.8%; Pred. No. 15;
RESULT 1086
ID ABL03436 standard; cDNA; 3790 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4790.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.6%; Score 38.2; DB 4; Length 3790;
Best Local Similarity 50.8%; Pred. No. 15;
RESULT 1087
ID ADK56219 standard; DNA; 651 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3602.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 1.6%; Score 38; DB 10; Length 651;
Best Local Similarity 53.3%; Pred. No. 5.5;
RESULT 1088
ID ADA68497 standard; DNA; 1359 BP.
DE Arabidopsis thaliana gene, SEQ ID 613.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 1.6%; Score 37.8; DB 8; Length 1359;
Best Local Similarity 52.2%; Pred. No. 10;
RESULT 1089
ID ABK33919 standard; DNA; 7001 BP.
DE Human DNA for staging of Astrocytomas #1.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.8; DB 6; Length 7001;
Best Local Similarity 48.4%; Pred. No. 30;
RESULT 1090
ID ADA20394 standard; DNA; 7001 BP.

DE Prostate tumour related genomic DNA sample #30.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.8; DB 8; Length 7001;
Best Local Similarity 48.4%; Pred. No. 30;
RESULT 1091
ID ADA84201 standard; DNA; 7001 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:59.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.8; DB 8; Length 7001;
Best Local Similarity 48.4%; Pred. No. 30;
RESULT 1092
ID ABA81167 standard; DNA; 121 BP.
DE UGT1 mutation correcting oligonucleotide SEQ ID NO: 4013.
PN WO200173002-A2.
PD 04-OCT-2001.
PA (UYDE) UNIV DELAWARE.
Query Match 1.6%; Score 37.6; DB 4; Length 121;
Best Local Similarity 59.3%; Pred. No. 2.3;
RESULT 1093
ID ABA81166 standard; DNA; 121 BP.
DE UGT1 mutation correcting oligonucleotide SEQ ID NO: 4012.
PN WO200173002-A2.
PD 04-OCT-2001.
PA (UYDE) UNIV DELAWARE.
Query Match 1.6%; Score 37.6; DB 4; Length 121;
Best Local Similarity 59.3%; Pred. No. 2.3;
RESULT 1094
ID ADM65492 standard; DNA; 482 BP.
DE NRY polymorphism detection primer #434.
PN US2003134285-A1.
PD 17-JUL-2003.
PA (OEFN/) OEFNER P J.
PA (UNDE/) UNDERHILL P A.
Query Match 1.6%; Score 37.6; DB 11; Length 482;
Best Local Similarity 54.3%; Pred. No. 5.9;
RESULT 1095
ID ADI81801 standard; cDNA; 492 BP.
DE A. thaliana array-associated cDNA SEQ ID 3.
PN DE10204843-A1.
PD 14-AUG-2003.
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
Query Match 1.6%; Score 37.6; DB 10; Length 492;
Best Local Similarity 55.3%; Pred. No. 6;
RESULT 1096
ID AAC67675 standard; cDNA; 1092 BP.
DE Human secreted protein cDNA sequence #45.
PN WO200058355-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37.6; DB 3; Length 1092;
Best Local Similarity 50.6%; Pred. No. 10;
RESULT 1097
ID ACA31552 standard; DNA; 1575 BP.

DE Prokaryotic essential gene #13209.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 37.6; DB 8; Length 1575;
Best Local Similarity 50.6%; Pred. No. 13;
RESULT 1098
ID ABL33217 standard; DNA; 6191 BP.
DE Human immune system associated gene SEQ ID NO: 1190.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.6; DB 6; Length 6191;
Best Local Similarity 49.0%; Pred. No. 32;
RESULT 1099
ID ABK31307 standard; DNA; 6191 BP.
DE Signal transduction associated gene modified complementary DNA #75.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.6; DB 6; Length 6191;
Best Local Similarity 49.0%; Pred. No. 32;
RESULT 1100
ID ABL70282 standard; DNA; 6191 BP.
DE Chemically treated cell signalling DNA sequence complementary to#86.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.6; DB 6; Length 6191;
Best Local Similarity 49.0%; Pred. No. 32;
RESULT 1101
ID ABN80161 standard; DNA; 6191 BP.
DE Human chemically modified disease associated gene SEQ ID NO 178.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.6; DB 6; Length 6191;
Best Local Similarity 49.0%; Pred. No. 32;
RESULT 1102
ID ABL33825 standard; DNA; 8771 BP.
DE Human immune system associated gene SEQ ID NO: 1798.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37.6; DB 6; Length 8771;
Best Local Similarity 46.0%; Pred. No. 40;
RESULT 1103
ID ACN44838 standard; DNA; 54169 BP.
DE Human genomic sequence hCG1766501.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 1.6%; Score 37.6; DB 11; Length 54169;
Best Local Similarity 45.3%; Pred. No. 1.4e+02;
RESULT 1104
Query Match 1.6%; Score 37.6; DB 2; Length 110000;
Best Local Similarity 47.1%; Pred. No. 2.2e+02;

RESULT 1105

ID ADH58564 standard; DNA; 139573 BP.
DE Human Na⁺-independent transporter-related transporter protein gene.
Query Match 1.6%; Score 37.6; DB 10; Length 139573;
Best Local Similarity 48.6%; Pred. No. 2.5e+02;

RESULT 1106

ID ABD32817 standard; DNA; 156416 BP.
DE Human cancer-associated genomic DNA HD17-001.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.6%; Score 37.6; DB 13; Length 156416;
Best Local Similarity 48.6%; Pred. No. 2.7e+02;

RESULT 1107

ID ACH76814 standard; DNA; 526 BP.
DE Human genome derived single exon probe #10009.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 1.6%; Score 37.4; DB 12; Length 526;
Best Local Similarity 52.2%; Pred. No. 7.1;

RESULT 1108

ID ACA22952 standard; DNA; 882 BP.
DE Prokaryotic essential gene #4609.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.6%; Score 37.4; DB 8; Length 882;
Best Local Similarity 60.2%; Pred. No. 10;

RESULT 1109

ID AAD55027 standard; DNA; 1365 BP.
DE Tulip pistil UDP-glucosyltransferase homologue gene, 114.
PN WO2002101013-A2.
PD 19-DEC-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PRAB/) PRABHU V.
Query Match 1.6%; Score 37.4; DB 10; Length 1365;
Best Local Similarity 53.8%; Pred. No. 13;

RESULT 1110

ID ABZ13579 standard; DNA; 1368 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1384.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.6%; Score 37.4; DB 6; Length 1368;
Best Local Similarity 53.0%; Pred. No. 13;

RESULT 1111

ID ADG87648 standard; cDNA; 1368 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #90.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZE BROOK J.

PA (WANG/) WANG X.
PA (DANG/) DANGL J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 37.4; DB 6; Length 1368;
Best Local Similarity 53.0%; Pred. No. 13;

RESULT 1112

ID ADG88159 standard; cDNA; 1368 BP.
DE A. thaliana RPP4-upregulated pathogen infection-related gene #601.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANGL J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 37.4; DB 6; Length 1368;
Best Local Similarity 53.0%; Pred. No. 13;

RESULT 1113

ID ADG87823 standard; cDNA; 1368 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #265.
PN WO200222675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANGL J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 37.4; DB 6; Length 1368;
Best Local Similarity 53.0%; Pred. No. 13;

RESULT 1114

ID ADA68049 standard; DNA; 1368 BP.
DE Arabidopsis thaliana gene, SEQ ID 304.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.6%; Score 37.4; DB 8; Length 1368;
Best Local Similarity 53.0%; Pred. No. 13;

RESULT 1115

ID AAD13669 standard; DNA; 1404 BP.
DE Arabidopsis thaliana glucosyltransferase (GTase) UGT71D1 DNA.
PN WO200159140-A1.
PD 16-AUG-2001.
PA (UYYO-) UNIV YORK.

Query Match 1.6%; Score 37.4; DB 4; Length 1404;
Best Local Similarity 51.5%; Pred. No. 14;

RESULT 1116

ID ABZ14405 standard; DNA; 1404 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2210.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.6%; Score 37.4; DB 6; Length 1404;
 Best Local Similarity 51.5%; Pred. No. 14;
 RESULT 1117
 ID AAC42644 standard; DNA; 1556 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36326.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.6%; Score 37.4; DB 3; Length 1556;
 Best Local Similarity 51.5%; Pred. No. 15;
 RESULT 1118
 ID ACA48184 standard; DNA; 2127 BP.
 DE Prokaryotic essential gene #29841.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 1.6%; Score 37.4; DB 8; Length 2127;
 Best Local Similarity 50.9%; Pred. No. 18;
 RESULT 1119
 ID AAX84332 standard; DNA; 5059 BP.
 DE Stealth virus nucleic acid clone, SEQ ID NO: 24.
 Query Match 1.6%; Score 37.4; DB 2; Length 5059;
 Best Local Similarity 12.9%; Pred. No. 32;
 RESULT 1120
 ID AAC76580 standard; cDNA; 5748 BP.
 DE Human ORFX ORF2135 polynucleotide sequence SEQ ID NO: 4269.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 1.6%; Score 37.4; DB 3; Length 5748;
 Best Local Similarity 49.2%; Pred. No. 35;
 RESULT 1121
 ID AAH98460 standard; cDNA; 6248 BP.
 DE Murine EST-derived coding sequence SEQ ID NO: 317.
 PN WO200154477-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 1.6%; Score 37.4; DB 4; Length 6248;
 Best Local Similarity 49.2%; Pred. No. 37;
 RESULT 1122
 ID AAS20800 standard; DNA; 48551 BP.
 DE Clostridium difficile DNA sequence upstream of ORF1.
 PN WO200194599-A1.
 PD 13-DEC-2001.
 PA (SMIT-) SMITTSKYDDSINSTITUTET.
 Query Match 1.6%; Score 37.4; DB 6; Length 48551;
 Best Local Similarity 53.0%; Pred. No. 1.4e+02;
 RESULT 1123
 Query Match 1.6%; Score 37.4; DB 2; Length 110000;
 Best Local Similarity 60.2%; Pred. No. 2.5e+02;
 RESULT 1124
 ID AAH71505 standard; cDNA; 310 BP.
 DE Human cervical cancer marker nucleic acid 2779.
 PN WO200142467-A2.
 PD 14-JUN-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 1.6%; Score 37.2; DB 4; Length 310;
 Best Local Similarity 53.4%; Pred. No. 5.8;

RESULT 1125

ID ADA68697 standard; DNA; 843 BP.

DE Rice gene, SEQ ID 2020.

PN WO2003000898-A1.

PD 03-JAN-2003.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.6%; Score 37.2; DB 8; Length 843;

Best Local Similarity 59.4%; Pred. No. 11;

RESULT 1126

ID ADJ11669 standard; DNA; 1110 BP.

DE Rice DNA modulated by post-transcriptional gene silencing SeqID 305.

PN US2003135888-A1.

PD 17-JUL-2003.

PA (ZHUT/) ZHU T.

PA (WANG/) WANG X.

PA (CHAN/) CHANG H.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZE BROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.

PA (PROV/) PROVART N.

PA (RICK/) RICKE D.

Query Match 1.6%; Score 37.2; DB 11; Length 1110;

Best Local Similarity 55.4%; Pred. No. 13;

RESULT 1127

ID AAV23108 standard; cDNA to mRNA; 1597 BP.

DE UDP-glucose:flavonoid 3,5-O-glucosyl transferase gene.

PN JP10113184-A.

PD 06-MAY-1998.

PA (TOLG) TOKYO GAS CO LTD.

Query Match 1.6%; Score 37.2; DB 2; Length 1597;

Best Local Similarity 54.3%; Pred. No. 17;

RESULT 1128

ID ADJ75971 standard; DNA; 2779 BP.

DE Marker gene SEQ ID NO:1223.

PN EP1394274-A2.

PD 03-MAR-2004.

PA (GENO-) GENOX RES INC.

Query Match 1.6%; Score 37.2; DB 12; Length 2779;

Best Local Similarity 47.8%; Pred. No. 25;

RESULT 1129

ID ACA47967 standard; DNA; 3502 BP.

DE Prokaryotic essential gene #29624.

PN WO200277183-A2.

PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match 1.6%; Score 37.2; DB 8; Length 3502;

Best Local Similarity 61.2%; Pred. No. 29;

RESULT 1130

ID ADM01769 standard; cDNA; 3524 BP.

DE Human cDNA of the invention SEQ ID NO:454.

PN EP1347046-A1.

PD 24-SEP-2003.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 1.6%; Score 37.2; DB 11; Length 3524;
 Best Local Similarity 56.6%; Pred. No. 29;
 RESULT 1131
 ID ABL05102 standard; cDNA; 3992 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 9788.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.6%; Score 37.2; DB 4; Length 3992;
 Best Local Similarity 61.2%; Pred. No. 31;
 RESULT 1132
 ID ACN44838 standard; DNA; 54169 BP.
 DE Human genomic sequence hCG1766501.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.6%; Score 37.2; DB 11; Length 54169;
 Best Local Similarity 51.2%; Pred. No. 1.8e+02;
 RESULT 1133
 ID ADD67054 standard; cDNA; 161280 BP.
 DE Human lung tumour-specific related cDNA, SEQ ID No 746.
 PN WO200292001-A2.
 PD 21-NOV-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 1.6%; Score 37.2; DB 10; Length 161280;
 Best Local Similarity 51.9%; Pred. No. 3.7e+02;
 RESULT 1134
 ID ADE88308 standard; cDNA; 161280 BP.
 DE Human lung tumour antigen cDNA #640.
 PN US2003118599-A1.
 PD 26-JUN-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 1.6%; Score 37.2; DB 10; Length 161280;
 Best Local Similarity 51.9%; Pred. No. 3.7e+02;
 RESULT 1135
 ID AAC74529 standard; cDNA; 510 BP.
 DE Human ORFX ORF84 polynucleotide sequence SEQ ID NO:167.
 PN WO200058473-A2.
 PD 05-OCT-2000.
 PA (CURA-) CURAGEN CORP.
 Query Match 1.6%; Score 37; DB 3; Length 510;
 Best Local Similarity 53.9%; Pred. No. 9.2;
 RESULT 1136
 ID ABX57387 standard; DNA; 537 BP.
 DE Arabidopsis thaliana polynucleotide #739.
 PN US2002040489-A1.
 PD 04-APR-2002.
 PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHEW A V.
 PA (LEDF/) LEDFORD B L.

PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.

Query Match 1.6%; Score 37; DB 10; Length 537;
Best Local Similarity 54.9%; Pred. No. 9.5;

RESULT 1137

ID ADK52732 standard; DNA; 753 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #115.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.

Query Match 1.6%; Score 37; DB 10; Length 753;
Best Local Similarity 54.9%; Pred. No. 12;

RESULT 1138

ID AAD55026 standard; DNA; 1365 BP.
DE Tulip pistil UDP-glucosyltransferase homologue gene, n21.
PN WO2002101013-A2.
PD 19-DEC-2002.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PRAB/) PRABHU V.

Query Match 1.6%; Score 37; DB 10; Length 1365;
Best Local Similarity 53.9%; Pred. No. 18;

RESULT 1139

ID ABZ14007 standard; DNA; 1446 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1812..
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.6%; Score 37; DB 6; Length 1446;
Best Local Similarity 54.9%; Pred. No. 18;

RESULT 1140

ID AAV49609 standard; cDNA; 1607 BP.
DE Potato solanidine UDP-glucose glucosyltransferase cDNA.
PN WO9834471-A1.
PD 13-AUG-1998.
PA (USDA) US SEC OF AGRIC.

Query Match 1.6%; Score 37; DB 2; Length 1607;
Best Local Similarity 48.0%; Pred. No. 20;

RESULT 1141

ID ADL14386 standard; DNA; 1670 BP.
DE DNA encoding a carnation glucosyltransferase enzyme SeqID 55.
PN WO2004018682-A1.
PD 04-MAR-2004.
PA (SUNR) SUNTORY LTD.
PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.

Query Match 1.6%; Score 37; DB 12; Length 1670;
Best Local Similarity 53.0%; Pred. No. 20;

RESULT 1142

ID AAS15727 standard; cDNA; 2145 BP.

DE DNA encoding sulfate anion transporter family related protein, NOV7.
PN WO200170978-A2.
PD 27-SEP-2001.
PA (CURA-) CURAGEN CORP.
Query Match 1.6%; Score 37; DB 4; Length 2145;
Best Local Similarity 53.9%; Pred. No. 24;
RESULT 1143
ID ADJ87760 standard; DNA; 2145 BP.
DE G-coupled protein receptor-related protein coding sequence #53.
PN WO2002102321-A2.
PD 27-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 1.6%; Score 37; DB 10; Length 2145;
Best Local Similarity 53.9%; Pred. No. 24;
RESULT 1144
ID ADO55995 standard; cDNA; 2145 BP.
DE DNA encoding human NOV7.
PN US2004058862-A1.
PD 25-MAR-2004.
PA (MAJU/) MAJUMDER K.
Query Match 1.6%; Score 37; DB 12; Length 2145;
Best Local Similarity 53.9%; Pred. No. 24;
RESULT 1145
ID AAD33658 standard; cDNA; 2600 BP.
DE Human TRICH-13 cDNA.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 1.6%; Score 37; DB 6; Length 2600;
Best Local Similarity 53.9%; Pred. No. 27;
RESULT 1146
ID AAL44757 standard; cDNA; 3435 BP.
DE Human transporter protein cDNA.
PN WO200188136-A2.
PD 22-NOV-2001.
PA (APPL-) APPLERA CORP.
Query Match 1.6%; Score 37; DB 6; Length 3435;
Best Local Similarity 53.9%; Pred. No. 33;
RESULT 1147
ID ABL33772 standard; DNA; 5666 BP.
DE Human immune system associated gene SEQ ID NO: 1745.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37; DB 6; Length 5666;
Best Local Similarity 53.9%; Pred. No. 46;
RESULT 1148
ID ABL33386 standard; DNA; 8064 BP.
DE Human immune system associated gene SEQ ID NO: 1359.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 37; DB 6; Length 8064;
Best Local Similarity 53.0%; Pred. No. 58;
RESULT 1149
ID AAL44758 standard; DNA; 8868 BP.
DE Human transporter protein gene.

PN WO200188136-A2.
 PD 22-NOV-2001.
 PA (APPL-) APPLERA CORP.
 Query Match 1.6%; Score 37; DB 6; Length 8868;
 Best Local Similarity 53.9%; Pred. No. 61;
 RESULT 1150
 ID AAK71442 standard; DNA; 23934 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26254.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
 RESULT 1151
 ID AAL36171 standard; DNA; 23934 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 2536.
 PN WO200155367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
 RESULT 1152
 ID AAL36179 standard; DNA; 23934 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 2544.
 PN WO200155367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
 RESULT 1153
 ID AAL04522 standard; DNA; 23934 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 7210.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
 RESULT 1154
 ID AAS28343 standard; DNA; 23934 BP.
 DE Genomic sequence #183 encoding for novel human respiratory antigen.
 PN WO200155448-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
 RESULT 1155
 ID ABL97446 standard; DNA; 23934 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2098.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 37; DB 4; Length 23934;
 Best Local Similarity 51.5%; Pred. No. 1.2e+02;
 RESULT 1156
 ID ABA19145 standard; DNA; 23934 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 11476.
 PN WO200159063-A2.

PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37; DB 5; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1157
ID ABX59167 standard; cDNA; 23934 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1511.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.6%; Score 37; DB 8; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1158
ID ABX59159 standard; cDNA; 23934 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1503.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 1.6%; Score 37; DB 8; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1159
ID ADG41539 standard; DNA; 23934 BP.
DE Human respiratory system associated genomic DNA seq id 777.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37; DB 10; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1160
ID ADI97313 standard; DNA; 23934 BP.
DE Human respiratory system associated polypeptide-related DNA SeqID777.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37; DB 11; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1161
ID ADJ29917 standard; DNA; 23934 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2544.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37; DB 12; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1162
ID ADJ29909 standard; DNA; 23934 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2536.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 1.6%; Score 37; DB 12; Length 23934;
Best Local Similarity 51.5%; Pred. No. 1.2e+02;
RESULT 1163

Query Match 1.6%; Score 37; DB 13; Length 110000;
 Best Local Similarity 49.7%; Pred. No. 3.3e+02;
 RESULT 1164
 ID ADB50767 standard; DNA; 512 BP.
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1309.
 PN WO2003065993-A2.
 PD 14-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 1.6%; Score 36.8; DB 10; Length 512;
 Best Local Similarity 50.6%; Pred. No. 11;
 RESULT 1165
 ID ABV57126 standard; cDNA; 550 BP.
 DE Human prostate expression marker cDNA 57117.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 1.6%; Score 36.8; DB 5; Length 550;
 Best Local Similarity 51.9%; Pred. No. 11;
 RESULT 1166
 ID AAT87010 standard; DNA; 618 BP.
 DE Nitrile hydratase alpha 29 kDa subunit encoding DNA.
 PN EP790310-A2.
 PD 20-AUG-1997.
 PA (MITK) MITSUI TOATSU CHEM INC.
 Query Match 1.6%; Score 36.8; DB 2; Length 618;
 Best Local Similarity 51.2%; Pred. No. 12;
 RESULT 1167
 ID ADP82951 standard; DNA; 618 BP.
 DE Nitrile hydratase alpha subunit coding sequence, SEQ ID 3.
 PN WO2004056990-A1.
 PD 08-JUL-2004.
 PA (MITA) MITSUI CHEM INC.
 Query Match 1.6%; Score 36.8; DB 12; Length 618;
 Best Local Similarity 51.2%; Pred. No. 12;
 RESULT 1168
 ID ADP83048 standard; DNA; 618 BP.
 DE Nitrile hydratase alpha subunit coding sequence, SEQ ID 100.
 PN WO2004056990-A1.
 PD 08-JUL-2004.
 PA (MITA) MITSUI CHEM INC.
 Query Match 1.6%; Score 36.8; DB 12; Length 618;
 Best Local Similarity 51.2%; Pred. No. 12;
 RESULT 1169
 ID AAZ95194 standard; DNA; 746 BP.
 DE Human UGT2B4 exon 2 nucleotide sequence.
 PN WO200006776-A1.
 PD 10-FEB-2000.
 PA (AXYS-) AXYS PHARM INC.
 Query Match 1.6%; Score 36.8; DB 3; Length 746;
 Best Local Similarity 54.4%; Pred. No. 14;
 RESULT 1170
 ID AAD49417 standard; DNA; 936 BP.
 DE Human serine/threonine protein kinase-like protein (STPKP) DNA #2.
 PN WO200283882-A2.
 PD 24-OCT-2002.
 PA (FARB) BAYER AG.
 Query Match 1.6%; Score 36.8; DB 8; Length 936;

Best Local Similarity 56.7%; Pred. No. 16;
 RESULT.1171
 ID AAH51490 standard; DNA; 1001 BP.
 DE Human UGT2B4 related DNA containing a biallelic polymorphism SEQ ID 381.
 PN WO200058508-A2.
 PD 05-OCT-2000.
 PA (GEST) GENSET.
 Query Match 1.6%; Score 36.8; DB 3; Length 1001;
 Best Local Similarity 54.4%; Pred. No. 17;
 RESULT 1172
 ID AAH51491 standard; DNA; 1001 BP.
 DE Human UGT2B4 related DNA containing a biallelic polymorphism SEQ ID 382.
 PN WO200058508-A2.
 PD 05-OCT-2000.
 PA (GEST) GENSET.
 Query Match 1.6%; Score 36.8; DB 3; Length 1001;
 Best Local Similarity 54.4%; Pred. No. 17;
 RESULT 1173
 ID AAD49416 standard; DNA; 1272 BP.
 DE Human serine/threonine protein kinase-like protein (STPKP) DNA #1.
 PN WO200283882-A2.
 PD 24-OCT-2002.
 PA (FARB) BAYER AG.
 Query Match 1.6%; Score 36.8; DB 8; Length 1272;
 Best Local Similarity 56.7%; Pred. No. 19;
 RESULT 1174
 ID AAS06744 standard; cDNA; 1275 BP.
 DE Polynucleotide sequence encoding human protein kinase #44.
 PN WO200138503-A2.
 PD 31-MAY-2001.
 PA (SUGE-) SUGEN INC.
 Query Match 1.6%; Score 36.8; DB 4; Length 1275;
 Best Local Similarity 56.7%; Pred. No. 19;
 RESULT 1175
 ID AAD49419 standard; DNA; 1275 BP.
 DE Human serine/threonine protein kinase-like protein (STPKP) DNA #4.
 PN WO200283882-A2.
 PD 24-OCT-2002.
 PA (FARB) BAYER AG.
 Query Match 1.6%; Score 36.8; DB 8; Length 1275;
 Best Local Similarity 56.7%; Pred. No. 19;
 RESULT 1176
 ID ABD33093 standard; cDNA; 1282 BP.
 DE Human cancer-associated (CA) cDNA HR07-006.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.6%; Score 36.8; DB 13; Length 1282;
 Best Local Similarity 56.7%; Pred. No. 20;
 RESULT 1177
 ID AAH68614 standard; cDNA; 1441 BP.
 DE Human protein HP10580 coding sequence.
 PN WO200142302-A1.
 PD 14-JUN-2001.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match 1.6%; Score 36.8; DB 5; Length 1441;
 Best Local Similarity 44.9%; Pred. No. 21;

RESULT 1178

ID ABK86975 standard; cDNA; 1473 BP.
DE Novel human protein (NHP) coding DNA.
PN WO200246428-A2.
PD 13-JUN-2002.
PA (LEXI-) LEXICON GENETICS INC.

Query Match 1.6%; Score 36.8; DB 6; Length 1473;
Best Local Similarity 56.7%; Pred. No. 21;

RESULT 1179

ID ACA37821 standard; DNA; 1650 BP.
DE Prokaryotic essential gene #19478.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match 1.6%; Score 36.8; DB 8; Length 1650;
Best Local Similarity 58.0%; Pred. No. 23;

RESULT 1180

ID ADQ85655 standard; cDNA; 1656 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2469.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.

Query Match 1.6%; Score 36.8; DB 12; Length 1656;
Best Local Similarity 44.9%; Pred. No. 23;

RESULT 1181

ID ADQ84269 standard; cDNA; 1656 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1083.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.

Query Match 1.6%; Score 36.8; DB 12; Length 1656;
Best Local Similarity 44.9%; Pred. No. 23;

RESULT 1182

ID ADQ86749 standard; cDNA; 1656 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3624.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.

Query Match 1.6%; Score 36.8; DB 13; Length 1656;
Best Local Similarity 44.9%; Pred. No. 23;

RESULT 1183

ID ACN40421 standard; cDNA; 1656 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326536, SEQ ID NO:5190.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.

Query Match 1.6%; Score 36.8; DB 13; Length 1656;
Best Local Similarity 44.9%; Pred. No. 23;

RESULT 1184

ID AAZ09324 standard; DNA; 1762 BP.
DE P. thermophila nitrila hydratase DNA.

PN EP943686-A2.
 PD 22-SEP-1999.
 PA (MITA) MITSUI CHEM INC.
 Query Match 1.6%; Score 36.8; DB 2; Length 1762;
 Best Local Similarity 51.2%; Pred. No. 24;
 RESULT 1185
 ID AAH64962 standard; cDNA; 1829 BP.
 DE Human secreted protein cDNA, SEQ ID NO: 238.
 PN WO200142451-A2.
 PD 14-JUN-2001.
 PA (GEST) GENSET.
 Query Match 1.6%; Score 36.8; DB 5; Length 1829;
 Best Local Similarity 44.9%; Pred. No. 25;
 RESULT 1186
 ID ACC00697 standard; cDNA; 1874 BP.
 DE Triticum aestivum oil trait related cDNA sequence SEQ ID NO:143.
 PN WO2003002751-A2.
 PD 09-JAN-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 1.6%; Score 36.8; DB 8; Length 1874;
 Best Local Similarity 51.9%; Pred. No. 25;
 RESULT 1187
 ID ADC23622 standard; cDNA; 1874 BP.
 DE cDNA encodes protein used to alter plant oil phenotype (SeqID 127).
 PN WO2003001902-A2.
 PD 09-JAN-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 Query Match 1.6%; Score 36.8; DB 10; Length 1874;
 Best Local Similarity 51.9%; Pred. No. 25;
 RESULT 1188
 ID ABX34648 standard; cDNA; 1960 BP.
 DE Human mddt cDNA SEQ ID 209.
 PN WO200279449-A2.
 PD 10-OCT-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 1.6%; Score 36.8; DB 8; Length 1960;
 Best Local Similarity 44.9%; Pred. No. 26;
 RESULT 1189
 ID AAD34298 standard; cDNA; 2060 BP.
 DE Human PKIN-1 cDNA.
 PN WO200218557-A2.
 PD 07-MAR-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 1.6%; Score 36.8; DB 6; Length 2060;.....
 Best Local Similarity 56.7%; Pred. No. 27;
 RESULT 1190
 ID ACA37512 standard; DNA; 2196 BP.
 DE Prokaryotic essential gene #19169.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 1.6%; Score 36.8; DB 8; Length 2196;
 Best Local Similarity 48.1%; Pred. No. 28;
 RESULT 1191
 ID AAS17862 standard; cDNA; 2598 BP.

DE Human protein kinase N cDNA.
 PN WO200188148-A2.
 PD 22-NOV-2001.
 PA (APPL-) APPLERA CORP.
 Query Match 1.6%; Score 36.8; DB 6; Length 2598;
 Best Local Similarity 56.7%; Pred. No. 31;
 RESULT 1192
 ID ABK10101 standard; cDNA; 2893 BP.
 DE Human cDNA encoding protein kinase 32374.
 PN WO200210401-A2.
 PD 07-FEB-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 1.6%; Score 36.8; DB 6; Length 2893;
 Best Local Similarity 56.7%; Pred. No. 33;
 RESULT 1193
 ID AAD49420 standard; DNA; 3124 BP.
 DE Human serine/threonine protein kinase-like protein (STPKP) DNA #5.
 PN WO200283882-A2.
 PD 24-OCT-2002.
 PA (FARB) BAYER AG.
 Query Match 1.6%; Score 36.8; DB 8; Length 3124;
 Best Local Similarity 56.7%; Pred. No. 35;
 RESULT 1194
 ID ADS89626 standard; DNA; 3862 BP.
 DE Oligonucleotide of the invention SEQ ID NO:642.
 PN WO2004035803-A2.
 PD 29-APR-2004.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36.8; DB 13; Length 3862;
 Best Local Similarity 49.5%; Pred. No. 41;
 RESULT 1195
 ID AAS63343 standard; DNA; 5464 BP.
 DE Chemically pretreated metabolism associated gene #38.
 PN WO200176451-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36.8; DB 6; Length 5464;
 Best Local Similarity 55.5%; Pred. No. 51;
 RESULT 1196
 ID AAA70152 standard; DNA; 6033 BP.
 DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:285.
 PN WO200025728-A2.
 PD 11-MAY-2000.
 PA (HOFF/) HOFFMAN S.
 PA (CARU/) CARUCCI D.
 PA (GARD/) GARDNER M.
 PA (VENT/) VENTER J C.
 Query Match 1.6%; Score 36.8; DB 3; Length 6033;
 Best Local Similarity 53.5%; Pred. No. 55;
 RESULT 1197
 ID ABL32369 standard; DNA; 9997 BP.
 DE Human immune system associated gene SEQ ID NO: 342.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36.8; DB 6; Length 9997;
 Best Local Similarity 46.8%; Pred. No. 76;

RESULT 1198

ID ABL34485 standard; DNA; 9997 BP.
DE Human metastasis associated gene SEQ ID NO: 38.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 9997;
Best Local Similarity 46.8%; Pred. No. 76;

RESULT 1199

ID ADS99746 standard; DNA; 9997 BP.
DE Complement of bisulphite treated metastasis-associated human gene #19.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 1.6%; Score 36.8; DB 7; Length 9997;
Best Local Similarity 46.8%; Pred. No. 76;

RESULT 1200

ID ABL33075 standard; DNA; 10254 BP.
DE Human immune system associated gene SEQ ID NO: 1048.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 10254;
Best Local Similarity 47.4%; Pred. No. 78;

RESULT 1201

ID ABL33262 standard; DNA; 12393 BP.
DE Human immune system associated gene SEQ ID NO: 1235.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 12393;
Best Local Similarity 50.0%; Pred. No. 88;

RESULT 1202

ID AAS45349 standard; DNA; 17421 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #27.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 4; Length 17421;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;

RESULT 1203

ID ABK28182 standard; DNA; 17421 BP.
DE DNA transcription associated complementary genomic DNA #28.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 17421;
Best Local Similarity 51.2%; Pred. No. 1.1e+02;

RESULT 1204

ID ABQ67059 standard; DNA; 34688 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 89.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36.8; DB 6; Length 34688;

Best Local Similarity 50.6%; Pred. No. 1.7e+02;
 RESULT 1205
 ID ABL34125 standard; DNA; 73334 BP.
 DE Human immune system associated gene SEQ ID NO: 2098.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36.8; DB 6; Length 73334;
 Best Local Similarity 48.2%; Pred. No. 2.9e+02;
 RESULT 1206
 ID ABL92319 standard; DNA; 73334 BP.
 DE Chemically treated DNA repair gene fragment complementary to#64.
 PN WO200181622-A2.
 PD 01-NOV-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36.8; DB 6; Length 73334;
 Best Local Similarity 48.2%; Pred. No. 2.9e+02;
 RESULT 1207
 ID AAI96898 standard; cDNA; 733 BP.
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2973.
 PN WO200166719-A1.
 PD 13-SEP-2001.
 PA (CHIB-) CHIBA PREFECTURE.
 PA (HISM) HISAMITSU PHARM CO LTD.
 Query Match 1.6%; Score 36.6; DB 4; Length 733;
 Best Local Similarity 56.1%; Pred. No. 15;
 RESULT 1208
 ID AAK65390 standard; DNA; 1238 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20202.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 36.6; DB 4; Length 1238;
 Best Local Similarity 55.0%; Pred. No. 22;
 RESULT 1209
 ID AAK70084 standard; DNA; 1238 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24896.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.6%; Score 36.6; DB 4; Length 1238;
 Best Local Similarity 55.0%; Pred. No. 22;
 RESULT 1210
 ID ABN70650 standard; DNA; 1257 BP.
 DE Streptococcus polynucleotide SEQ ID NO 9213.
 PN WO200234771-A2.
 PD 02-MAY-2002.
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 Query Match 1.6%; Score 36.6; DB 6; Length 1257;
 Best Local Similarity 47.9%; Pred. No. 22;
 RESULT 1211
 ID ACA50557 standard; DNA; 1260 BP.
 DE Prokaryotic essential gene #32214.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.

Query Match 1.6%; Score 36.6; DB 8; Length 1260;
 Best Local Similarity 47.9%; Pred. No. 22;
 RESULT 1212
 ID ADE25650 standard; cDNA; 1830 BP.
 DE Human cDNA differentially expressed in foam cells #54.
 PN US2003194721-A1.
 PD 16-OCT-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 1.6%; Score 36.6; DB 10; Length 1830;
 Best Local Similarity 56.1%; Pred. No. 28;
 RESULT 1213
 ID ADN04923 standard; cDNA; 3400 BP.
 DE Antipsoriatic cDNA sequence #676.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 36.6; DB 12; Length 3400;
 Best Local Similarity 56.1%; Pred. No. 43;
 RESULT 1214
 ID ADF76479 standard; cDNA; 3401 BP.
 DE Novel human secreted and transmembrane protein cDNA SeqID 153.
 PN WO2003072035-A2.
 PD 04-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 36.6; DB 10; Length 3401;
 Best Local Similarity 56.1%; Pred. No. 43;
 RESULT 1215
 ID ADK51974 standard; cDNA; 3401 BP.
 DE Human atopic dermatitis/psoriasis-associated cDNA #7.
 PN WO2004016785-A1.
 PD 26-FEB-2004.
 PA (GENO-) GENOX RES INC.
 PA (UYJU-) UNIV JUNTENDO.
 Query Match 1.6%; Score 36.6; DB 12; Length 3401;
 Best Local Similarity 56.1%; Pred. No. 43;
 RESULT 1216
 ID ADR14492 standard; DNA; 3401 BP.
 DE Human NF-kappaB pathway-associated gene SeqID493.
 PN WO2004065577-A2.
 PD 05-AUG-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 1.6%; Score 36.6; DB 13; Length 3401;
 Best Local Similarity 56.1%; Pred. No. 43;
 RESULT 1217
 ID ADP25120 standard; cDNA; 3401 BP.
 DE PRO polypeptide encoding cDNA SEQ ID NO:2298.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 1.6%; Score 36.6; DB 13; Length 3401;
 Best Local Similarity 56.1%; Pred. No. 43;
 RESULT 1218
 ID AAK77709 standard; DNA; 4028 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32521.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.6%; Score 36.6; DB 4; Length 4028;
 Best Local Similarity 56.1%; Pred. No. 48;
 RESULT 1219
 ID ABX63656 standard; cDNA; 4040 BP.
 DE Human cDNA #656 differentially expressed in activated vascular tissue.
 PN US2002137081-A1.
 PD 26-SEP-2002.
 PA (BAND/) BANDMAN O.
 Query Match 1.6%; Score 36.6; DB 8; Length 4040;
 Best Local Similarity 56.1%; Pred. No. 48;
 RESULT 1220
 ID AAA70225 standard; DNA; 4056 BP.
 DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:358.
 PN WO200025728-A2.
 PD 11-MAY-2000.
 PA (HOFF/) HOFFMAN S.
 PA (CARU/) CARUCCI D.
 PA (GARD/) GARDNER M.
 PA (VENT/) VENTER J C.
 Query Match 1.6%; Score 36.6; DB 3; Length 4056;
 Best Local Similarity 45.8%; Pred. No. 48;
 RESULT 1221
 ID AAS01528 standard; cDNA; 4541 BP.
 DE Human secretory molecule cDNA sptm #18.
 PN WO200123558-A2.
 PD 05-APR-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 1.6%; Score 36.6; DB 4; Length 4541;
 Best Local Similarity 55.6%; Pred. No. 52;
 RESULT 1222
 ID AAS01147 standard; DNA; 6233 BP.
 DE Interferon induced nucleic acid, IFN2.
 PN WO200118208-A2.
 PD 15-MAR-2001.
 PA (CURA-) CURAGEN CORP.
 PA (BIOJ) BIOGEN INC.
 Query Match 1.6%; Score 36.6; DB 4; Length 6233;
 Best Local Similarity 56.1%; Pred. No. 64;
 RESULT 1223
 ID ABN89476 standard; cDNA; 19806 BP.
 DE Human dehydrogenase genomic DNA SEQ ID NO:3.
 PN WO200250255-A2.
 PD 27-JUN-2002.
 PA (PEKE) PE CORP NY.
 Query Match 1.6%; Score 36.6; DB 6; Length 19806;
 Best Local Similarity 51.5%; Pred. No. 1.4e+02;
 RESULT 1224
 ID ABD32550 standard; DNA; 37180 BP.
 DE Mouse cancer-associated genomic DNA MD7-053.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.6%; Score 36.6; DB 13; Length 37180;
 Best Local Similarity 51.5%; Pred. No. 2.1e+02;
 RESULT 1225
 Query Match 1.6%; Score 36.6; DB 13; Length 110000;
 Best Local Similarity 43.5%; Pred. No. 4.3e+02;

RESULT 1226

ID ADJ43093 standard; cDNA; 585 BP.
 DE Plant cDNA #4093.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZE BROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 36.4; DB 12; Length 585;
 Best Local Similarity 51.2%; Pred. No. 15;

RESULT 1227

ID ADJ43094 standard; cDNA; 718 BP.
 DE Plant cDNA #4094.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZE BROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 36.4; DB 12; Length 718;
 Best Local Similarity 51.2%; Pred. No. 17;

RESULT 1228

ID ADJ41807 standard; cDNA; 761 BP.
 DE Plant cDNA #2807.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZE BROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 36.4; DB 12; Length 761;
 Best Local Similarity 51.2%; Pred. No. 18;

RESULT 1229

ID ADJ41799 standard; cDNA; 864 BP.
 DE Plant cDNA #2799.

PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZE BROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.

Query Match 1.6%; Score 36.4; DB 12; Length 864;
Best Local Similarity 53.5%; Pred. No. 20;

RESULT 1230

ID AAF57028 standard; cDNA; 1077 BP.
DE P. furiosus RFA polypeptide encoding cDNA.
PN WO200109347-A2.
PD 08-FEB-2001.
PA (STRA-) STRATAGENE.

Query Match 1.6%; Score 36.4; DB 4; Length 1077;
Best Local Similarity 53.5%; Pred. No. 23;

RESULT 1231

ID ACA10126 standard; cDNA; 1266 BP.
DE Human NOVX polynucleotide #16.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.

Query Match 1.6%; Score 36.4; DB 8; Length 1266;
Best Local Similarity 56.1%; Pred. No. 25;

RESULT 1232

ID ADE40267 standard; cDNA; 1266 BP.
DE Human NOV39b cDNA - SEQ ID 173.
PN WO2003064589-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.

Query Match 1.6%; Score 36.4; DB 10; Length 1266;
Best Local Similarity 56.1%; Pred. No. 25;

RESULT 1233

ID ADO08284 standard; cDNA; 1266 BP.
DE Human NOVX polynucleotide #16.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.

PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.

Query Match 1.6%; Score 36.4; DB 12; Length 1266;
Best Local Similarity 56.1%; Pred. No. 25;

RESULT 1234

ID ADC08349 standard; DNA; 2199 BP.
DE Rice DNA sequence Seq ID654 related to grain filling.
PN WO2003000905-A2.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.6%; Score 36.4; DB 10; Length 2199;
Best Local Similarity 52.1%; Pred. No. 37;

RESULT 1235

ID AAC42784 standard; DNA; 2295 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36836.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 1.6%; Score 36.4; DB 3; Length 2295;
Best Local Similarity 50.0%; Pred. No. 38;

RESULT 1236

ID AAC48369 standard; DNA; 2439 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57229.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 1.6%; Score 36.4; DB 3; Length 2439;
Best Local Similarity 50.0%; Pred. No. 39;

RESULT 1237

ID AAS45488 standard; DNA; 6620 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #97.
PN WO200168911-A2.
PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.6%; Score 36.4; DB 4; Length 6620;
Best Local Similarity 51.4%; Pred. No. 76;

RESULT 1238

ID ABK28416 standard; DNA; 6620 BP.
DE DNA transcription associated complementary genomic DNA #145.
PN WO200192565-A2.
PD 06-DEC-2001.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.6%; Score 36.4; DB 6; Length 6620;
Best Local Similarity 51.4%; Pred. No. 76;

RESULT 1239

ID ABN80279 standard; DNA; 6620 BP.
 DE Human chemically modified disease associated gene SEQ ID NO.296.
 PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36.4; DB 6; Length 6620;
 Best Local Similarity 51.4%; Pred. No. 76;
 RESULT 1240
 ID ABL19228 standard; DNA; 10078 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9157.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.6%; Score 36.4; DB 4; Length 10078;
 Best Local Similarity 52.7%; Pred. No. 1e+02;
 RESULT 1241
 ID ABL33110 standard; DNA; 10957 BP.
 DE Human immune system associated gene SEQ ID NO: 1083.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36.4; DB 6; Length 10957;
 Best Local Similarity 49.6%; Pred. No. 1.1e+02;
 RESULT 1242
 ID ABL33933 standard; DNA; 19734 BP.
 DE Human immune system associated gene SEQ ID NO: 1906.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36.4; DB 6; Length 19734;
 Best Local Similarity 47.4%; Pred. No. 1.6e+02;
 RESULT 1243
 Query Match 1.6%; Score 36.4; DB 12; Length 110000;
 Best Local Similarity 56.8%; Pred. No. 4.9e+02;
 RESULT 1244
 ID ABD33534 standard; DNA; 153995 BP.
 DE Murine cancer-associated (CA) gene MD07-106.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.6%; Score 36.4; DB 13; Length 153995;
 Best Local Similarity 50.0%; Pred. No. 6.1e+02;
 RESULT 1245
 ID ADL08119 standard; DNA; 158091 BP.
 DE Human gene associated with low HDL-C LIPC #1.
 PN US2004043389-A1.
 PD 04-MAR-2004.
 PA (VITI-) VITIVITY INC.
 Query Match 1.6%; Score 36.4; DB 12; Length 158091;
 Best Local Similarity 51.9%; Pred. No. 6.2e+02;
 RESULT 1246
 ID ADS36450 standard; DNA; 321019 BP.
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1664.
 PN WO2004083403-A2.
 PD 30-SEP-2004.
 PA (APPL-) APPLERA CORP..
 Query Match 1.6%; Score 36.4; DB 13; Length 321019;

Best Local Similarity 49.5%; Pred. No. 9.8e+02;

RESULT 1247

ID ABD32707 standard; DNA; 329019 BP.

DE Human cancer-associated genomic DNA HD14-043.

PN WO2004074320-A2.

PD 02-SEP-2004.

PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 1.6%; Score 36.4; DB 13; Length 329019;

Best Local Similarity 49.5%; Pred. No. 9.9e+02;

RESULT 1248

ID ABQ65858 standard; DNA; 667 BP.

DE Arabidopsis thaliana polynucleotide SEQ ID NO 435.

PN US2002059663-A1.

PD 16-MAY-2002.

PA (GORL/) GORLACH J.

PA (ANYY/) AN Y.

PA (HAMI/) HAMILTON C M.

PA (PRIC/) PRICE J L.

PA (RAIN/) RAINES T M.

PA (YUYU/) YU Y.

PA (RAME/) RAMEAKA J G.

PA (PAGE/) PAGE A.

PA (MATH/) MATHEW A V.

PA (LEDF/) LEDFORD B L.

PA (WOES/) WOESSNER J P.

PA (HAAS/) HAAS W D.

PA (GARC/) GARCIA C A.

PA (KRIC/) KRICKER M.

PA (SLAT/) SLATER T.

PA (DAVI/) DAVIS K R.

PA (ALLE/) ALLEN K.

PA (HOFF/) HOFFMAN N.

PA (HURB/) HURBAN P.

Query Match 1.6%; Score 36.2; DB 6; Length 667;

Best Local Similarity 52.3%; Pred. No. 19;

RESULT 1249

ID AAX20324 standard; DNA; 1300 BP.

DE Borrelia burgdorferi polynucleotide sequence #77.

PN WO9858943-A1.

PD 30-DEC-1998.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (MEDI-) MEDIMMUNE INC.

Query Match 1.6%; Score 36.2; DB 2; Length 1300;

Best Local Similarity 47.9%; Pred. No. 30;

RESULT 1250

ID ABL06636 standard; cDNA; 2878 BP..

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 14390.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 1.6%; Score 36.2; DB 4; Length 2878;

Best Local Similarity 44.1%; Pred. No. 50;

RESULT 1251

ID AAS51614 standard; DNA; 2988 BP.

DE Staphylococcus aureus DNA for cellular proliferation protein #31.

PN WO200170955-A2.

PD 27-SEP-2001.

PA (ELIT-) ELITRA PHARM INC.

Query Match 1.6%; Score 36.2; DB 4; Length 2988;

Best Local Similarity 47.2%; Pred. No. 52;

RESULT 1252

ID AAS54406 standard; DNA; 3030 BP.

DE Staphylococcus aureus DNA for cellular proliferation protein #718.

PN WO200170955-A2.

PD 27-SEP-2001.

PA (ELIT-) ELITRA PHARM INC.

Query Match 1.6%; Score 36.2; DB 4; Length 3030;

Best Local Similarity 47.2%; Pred. No. 52;

RESULT 1253

ID AAA26288 standard; cDNA; 3129 BP.

DE Human secreted protein gene 8 SEQ ID NO:18.

PN WO200011014-A1.

PD 02-MAR-2000.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.6%; Score 36.2; DB 3; Length 3129;

Best Local Similarity 49.0%; Pred. No. 53;

RESULT 1254

ID ABL17727 standard; DNA; 3507 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4654.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 1.6%; Score 36.2; DB 4; Length 3507;

Best Local Similarity 53.1%; Pred. No. 57;

RESULT 1255

ID ABL17726 standard; DNA; 5815 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4651.

PN WO200171042-A2.

PD 27-SEP-2001.

PA (PEKE) PE CORP NY.

Query Match 1.6%; Score 36.2; DB 4; Length 5815;

Best Local Similarity 53.1%; Pred. No. 80;

RESULT 1256

ID AAV58938 standard; DNA; 10095 BP.

DE Mycobacterium tuberculosis embCAB operon.

PN WO9841533-A1.

PD 24-SEP-1998.

PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.

Query Match 1.6%; Score 36.2; DB 2; Length 10095;

Best Local Similarity 51.6%; Pred. No. 1.2e+02;

RESULT 1257

ID ADJ12590 standard; DNA; 11122 BP.

DE DNA fragment of a BAC clone that encodes a human secreted protein Seq444.

PN US2004010132-A1.

PD 15-JAN-2004.

PA (ROSE/) ROSEN C A.

PA (BREW/) BREWER L A.

PA (DUAN/) DUAN R D.

PA (RUBE/) RUBEN S M.

PA (FLOR/) FLORENCE K A.

PA (GREE/) GREENE J M.

PA (YOUN/) YOUNG P E.

PA (FERR/) FERRIE A M.

PA (YUGG/) YU G.

PA (FLOR/) FLORENCE C.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H.

Query Match 1.6%; Score 36.2; DB 12; Length 11122;
Best Local Similarity 49.0%; Pred. No. 1.2e+02;

RESULT 1258

ID ADJ12540 standard; DNA; 11122 BP.
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq394.
PN US2004010132-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (DUAN/) DUAN R D.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (GREE/) GREENE J M.
PA (YOUN/) YOUNG P E.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (FLOR/) FLORENCE C.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H.

Query Match 1.6%; Score 36.2; DB 12; Length 11122;
Best Local Similarity 49.0%; Pred. No. 1.2e+02;

RESULT 1259

ID AAS29967 standard; DNA; 11172 BP.
DE Human lung antigen genomic DNA #37.
PN WO200155303-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.6%; Score 36.2; DB 5; Length 11172;
Best Local Similarity 50.9%; Pred. No. 1.2e+02;

RESULT 1260

ID ADB33304 standard; DNA; 11172 BP.
DE Human novel lung related polypeptide DNA SEQ ID NO 231.
PN US2003054368-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.6%; Score 36.2; DB 10; Length 11172;
Best Local Similarity 50.9%; Pred. No. 1.2e+02;

RESULT 1261

ID ABL32299 standard; DNA; 12507 BP.
DE Human immune system associated gene SEQ ID NO: 272.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.6%; Score 36.2; DB 6; Length 12507;
Best Local Similarity 49.2%; Pred. No. 1.3e+02;

RESULT 1262

ID ADD48574 standard; DNA; 28564 BP.
DE Human gene AL022727, SEQ ID NO 14280.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

Query Match 1.6%; Score 36.2; DB 10; Length 28564;
Best Local Similarity 52.3%; Pred. No. 2.3e+02;

RESULT 1263

ID ADD46575 standard; DNA; 28564 BP.
DE Human gene AL022727, SEQ ID NO 12257.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

Query Match 1.6%; Score 36.2; DB 10; Length 28564;
Best Local Similarity 52.3%; Pred. No. 2.3e+02;

RESULT 1264

ID ABQ67006 standard; DNA; 33053 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 36.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match 1.6%; Score 36.2; DB 6; Length 33053;
Best Local Similarity 46.0%; Pred. No. 2.5e+02;

RESULT 1265

ID AAD55116 standard; DNA; 98829 BP.
DE Human ACE reference DNA (GI 13027555).
PN WO2003020118-A2.
PD 13-MAR-2003.
PA (VITI-) VITIVITY INC.

Query Match 1.6%; Score 36.2; DB 9; Length 98829;
Best Local Similarity 50.9%; Pred. No. 5.3e+02;

RESULT 1266

Query Match 1.6%; Score 36.2; DB 4; Length 110000;
Best Local Similarity 51.6%; Pred. No. 5.6e+02;

RESULT 1267

Query Match 1.6%; Score 36.2; DB 4; Length 110000;
Best Local Similarity 51.6%; Pred. No. 5.6e+02;

RESULT 1268

ID ADH77123 standard; DNA; 126001 BP.
DE Human PAZ/PIWI domain-containing protein polynucleotide #3.
PN US2003232442-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.

Query Match 1.6%; Score 36.2; DB 12; Length 126001;
Best Local Similarity 53.1%; Pred. No. 6.2e+02;

RESULT 1269

ID ADS69085 standard; cDNA; 279 BP.
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 4101.
PN US2003237110-A9.
PD 25-DEC-2003.
PA (INCY-) INCYTE PHARM INC.

Query Match 1.6%; Score 36; DB 7; Length 279;
Best Local Similarity 51.6%; Pred. No. 12;

RESULT 1270

ID AAQ14776 standard; DNA; 303 BP.
DE IGF-I under alpha-S1-casein control regions.
PN EP451823-A.
PD 16-OCT-1991.
PA (CONE) CONSORTIUM ELEKTROCHEM IND.

Query Match 1.6%; Score 36; DB 2; Length 303;
Best Local Similarity 62.0%; Pred. No. 13;

RESULT 1271

ID ACH75803 standard; DNA; 527 BP.

DE Human genome derived single exon probe #8998.
 PN US2003194704-A1.
 PD 16-OCT-2003.
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 Query Match 1.6%; Score 36; DB 12; Length 527;
 Best Local Similarity 50.0%; Pred. No. 19;
 RESULT 1272
 ID AAA51052 standard; DNA; 719 BP.
 DE Soybean SAMS promoter fragment.
 PN WO200037662-A2.
 PD 29-JUN-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.6%; Score 36; DB 3; Length 719;
 Best Local Similarity 53.6%; Pred. No. 23;
 RESULT 1273
 ID ABD04376 standard; DNA; 801 BP.
 DE Pseudomonas aeruginosa polynucleotide #2980.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.6%; Score 36; DB 11; Length 801;
 Best Local Similarity 52.7%; Pred. No. 25;
 RESULT 1274
 ID ACA38703 standard; DNA; 1170 BP.
 DE Prokaryotic essential gene #20360.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 1.6%; Score 36; DB 8; Length 1170;
 Best Local Similarity 51.2%; Pred. No. 32;
 RESULT 1275
 ID ACA40348 standard; DNA; 1227 BP.
 DE Prokaryotic essential gene #22005.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 1.6%; Score 36; DB 8; Length 1227;
 Best Local Similarity 51.2%; Pred. No. 33;
 RESULT 1276
 ID AAA51042 standard; DNA; 1314 BP.
 DE Soybean SAMS promoter region.
 PN WO200037662-A2.
 PD 29-JUN-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.6%; Score 36; DB 3; Length 1314;
 Best Local Similarity 53.6%; Pred. No. 34;
 RESULT 1277
 ID ACA30500 standard; DNA; 1536 BP.
 DE Prokaryotic essential gene #12157.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 1.6%; Score 36; DB 8; Length 1536;
 Best Local Similarity 56.9%; Pred. No. 38;
 RESULT 1278

ID AAA51051 standard; DNA; 1574 BP.
 DE Soybean S-adenosyl-L-methionine synthetase promoter fragment.
 PN WO200037662-A2.
 PD 29-JUN-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.6%; Score 36; DB 3; Length 1574;
 Best Local Similarity 53.6%; Pred. No. 39;
 RESULT 1279
 ID ABD04100 standard; DNA; 1785 BP.
 DE Pseudomonas aeruginosa polynucleotide #2704.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.6%; Score 36; DB 11; Length 1785;
 Best Local Similarity 52.7%; Pred. No. 42;
 RESULT 1280
 ID ABL41494 standard; cDNA; 1986 BP.
 DE Human hypertension-related gene HRG-1 cDNA.
 PN CN1181420-A.
 PD 13-MAY-1998.
 PA (UYBE-) UNIV BEIJING MEDICAL.
 Query Match 1.6%; Score 36; DB 6; Length 1986;
 Best Local Similarity 55.6%; Pred. No. 45;
 RESULT 1281
 ID AAA51050 standard; DNA; 2165 BP.
 DE Soybean S-adenosyl-L-methionine synthetase promoter fragment.
 PN WO200037662-A2.
 PD 29-JUN-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.6%; Score 36; DB 3; Length 2165;
 Best Local Similarity 53.6%; Pred. No. 48;
 RESULT 1282
 ID AAA51038 standard; DNA; 2336 BP.
 DE Soybean S-adenosyl-L-methionine synthetase genomic DNA.
 PN WO200037662-A2.
 PD 29-JUN-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.6%; Score 36; DB 3; Length 2336;
 Best Local Similarity 53.6%; Pred. No. 50;
 RESULT 1283
 ID AAA51055 standard; DNA; 3684 BP.
 DE SAMS promoter::ATPS DNA fragment.
 PN WO200037662-A2.
 PD 29-JUN-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.6%; Score 36; DB 3; Length 3684;
 Best Local Similarity 53.6%; Pred. No. 68;
 RESULT 1284
 ID AAA51056 standard; DNA; 3963 BP.
 DE SAMS promoter::CGS1 DNA fragment.
 PN WO200037662-A2.
 PD 29-JUN-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.6%; Score 36; DB 3; Length 3963;
 Best Local Similarity 53.6%; Pred. No. 72;
 RESULT 1285
 ID ADR20217 standard; DNA; 3979 BP.

DE Soybean expression cassette nucleotide sequence SEQ ID NO:90.
PN WO2004071467-A2.
PD 26-AUG-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 13; Length 3979;
Best Local Similarity 53.6%; Pred. No. 72;
RESULT 1286
ID AAA51054 standard; DNA; 3985 BP.
DE SAMS promoter::GUS::3' Nos DNA fragment.
PN WO200037662-A2.
PD 29-JUN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 1.6%; Score 36; DB 3; Length 3985;
Best Local Similarity 53.6%; Pred. No. 72;
RESULT 1287
ID AAC85792 standard; cDNA; 4550 BP.
DE hMfn2 cDNA.
PN WO200125274-A1.
PD 12-APR-2001.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 1.6%; Score 36; DB 4; Length 4550;
Best Local Similarity 55.6%; Pred. No. 78;
RESULT 1288
ID ABX96873 standard; DNA; 4550 BP.
DE DNA encoding the human mitofusin 2, Mfn2.
PN US2002168673-A1.
PD 14-NOV-2002.
PA (FULL/) FULLER M T.
PA (HALE/) HALES K G.
PA (SANT/) SANTEL A H.
Query Match 1.6%; Score 36; DB 8; Length 4550;
Best Local Similarity 55.6%; Pred. No. 78;
RESULT 1289
ID AAV69110 standard; DNA; 5064 BP.
DE Neisseria meningitidis ctrA-gale region genomic DNA.
PN WO9845312-A1.
PD 15-OCT-1998.
PA (UYEM-) UNIV EMORY.
Query Match 1.6%; Score 36; DB 2; Length 5064;
Best Local Similarity 46.4%; Pred. No. 84;
RESULT 1290
ID ABL33976 standard; DNA; 8456 BP.
DE Human immune system associated gene SEQ ID NO: 1949.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36; DB 6; Length 8456;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
RESULT 1291
ID ABQ66990 standard; DNA; 9118 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 20.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.6%; Score 36; DB 6; Length 9118;
Best Local Similarity 48.5%; Pred. No. 1.2e+02;
RESULT 1292

ID ABN80049 standard; DNA; 9543 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 66.
 PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36; DB 6; Length 9543;
 Best Local Similarity 48.5%; Pred. No. 1.3e+02;
 RESULT 1293
 ID ABL32976 standard; DNA; 18512 BP.
 DE Human immune system associated gene SEQ ID NO: 949.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.6%; Score 36; DB 6; Length 18512;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 RESULT 1294
 Query Match 1.6%; Score 36; DB 13; Length 89736;
 Best Local Similarity 49.5%; Pred. No. 5.7e+02;
 RESULT 1295
 ID ABD32711 standard; DNA; 94781 BP.
 DE Mouse cancer-associated genomic DNA MD14-044.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.6%; Score 36; DB 13; Length 94781;
 Best Local Similarity 52.7%; Pred. No. 5.9e+02;
 RESULT 1296
 Query Match 1.6%; Score 36; DB 4; Length 110000;
 Best Local Similarity 51.2%; Pred. No. 6.5e+02;
 RESULT 1297
 Query Match 1.6%; Score 36; DB 4; Length 110000;
 Best Local Similarity 51.2%; Pred. No. 6.5e+02;
 RESULT 1298
 ID AAV86185 standard; cDNA; 600 BP.
 DE EST clone J635.
 PN WO9845435-A2.
 PD 15-OCT-1998.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 35.8; DB 2; Length 600;
 Best Local Similarity 17.4%; Pred. No. 23;
 RESULT 1299
 ID ADC92334 standard; DNA; 831 BP.
 DE E. faecium DNA sequence SEQ ID 1961.
 PN US6583275-B1.
 PD 24-JUN-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.5%; Score 35.8; DB 10; Length 831;
 Best Local Similarity 53.1%; Pred. No. 29;
 RESULT 1300
 ID ABL25777 standard; DNA; 1395 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28804.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.5%; Score 35.8; DB 4; Length 1395;
 Best Local Similarity 55.1%; Pred. No. 41;
 RESULT 1301

ID AAQ74684 standard; cDNA; 1650 BP.
 DE Early Ripening Tomato protein ERT1b gene.
 PN WO9421794-A1.
 PD 29-SEP-1994.
 PA (ZENE) ZENECA LTD.
 Query Match 1.5%; Score 35.8; DB 2; Length 1650;
 Best Local Similarity 52.3%; Pred. No. 46;
 RESULT 1302
 ID ACA30586 standard; DNA; 1899 BP.
 DE Prokaryotic essential gene #12243.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 1.5%; Score 35.8; DB 8; Length 1899;
 Best Local Similarity 49.7%; Pred. No. 50;
 RESULT 1303
 ID ABL25776 standard; DNA; 3894 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28801.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.5%; Score 35.8; DB 4; Length 3894;
 Best Local Similarity 55.1%; Pred. No. 81;
 RESULT 1304
 ID ABK31378 standard; DNA; 5338 BP.
 DE Signal transduction associated gene modified DNA #111.
 PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.8; DB 6; Length 5338;
 Best Local Similarity 48.7%; Pred. No. 1e+02;
 RESULT 1305
 ID ABL70329 standard; DNA; 5338 BP.
 DE Chemically treated cell signalling DNA sequence#110.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.8; DB 6; Length 5338;
 Best Local Similarity 48.7%; Pred. No. 1e+02;
 RESULT 1306
 ID AAS61280 standard; DNA; 5338 BP.
 DE Human gene regulation-associated gene oligonucleotide #235.
 PN WO200177375-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.8; DB 6; Length 5338;
 Best Local Similarity 48.7%; Pred. No. 1e+02;
 RESULT 1307
 ID ABL33491 standard; DNA; 8392 BP.
 DE Human immune system associated gene SEQ ID NO: 1464.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.8; DB 6; Length 8392;
 Best Local Similarity 47.8%; Pred. No. 1.4e+02;
 RESULT 1308
 ID ABL32795 standard; DNA; 8951 BP.

DE Human immune system associated gene SEQ ID NO: 768.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.8; DB 6; Length 8951;
 Best Local Similarity 55.1%; Pred. No. 1.4e+02;
 RESULT 1309
 ID AAK75286 standard; DNA; 10055 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30098.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.8; DB 4; Length 10055;
 Best Local Similarity 48.3%; Pred. No. 1.5e+02;
 RESULT 1310
 ID AAS45328 standard; DNA; 11735 BP.
 DE Chemically pretreated genomic DNA associated with cell cycle #17.
 PN WO200168911-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.8; DB 4; Length 11735;
 Best Local Similarity 46.6%; Pred. No. 1.7e+02;
 RESULT 1311
 ID ABK28167 standard; DNA; 11735 BP.
 DE DNA transcription associated genomic DNA #21.
 PN WO200192565-A2.
 PD 06-DEC-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.8; DB 6; Length 11735;
 Best Local Similarity 46.6%; Pred. No. 1.7e+02;
 RESULT 1312
 ID AAS61141 standard; DNA; 11735 BP.
 DE Human gene regulation-associated gene oligonucleotide #96.
 PN WO200177375-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.8; DB 6; Length 11735;
 Best Local Similarity 46.6%; Pred. No. 1.7e+02;
 RESULT 1313
 ID AAK65368 standard; DNA; 18564 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20180.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.8; DB 4; Length 18564;
 Best Local Similarity 56.3%; Pred. No. 2.3e+02;
 RESULT 1314
 ID ABZ74461 standard; DNA; 18564 BP.
 DE Secreted protein gene 300 genomic fragment HSQDO85, SEQ ID NO:1608.
 PN WO200277013-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.8; DB 8; Length 18564;
 Best Local Similarity 56.3%; Pred. No. 2.3e+02;
 RESULT 1315
 ID ADA98881 standard; DNA; 18564 BP.
 DE Human secreted protein-related DNA sequence #474.

PN WO2003004623-A2.
 PD 16-JAN-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.8; DB 8; Length 18564;
 Best Local Similarity 56.3%; Pred. No. 2.3e+02;
 RESULT 1316
 ID AAK75287 standard; DNA; 18855 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30099.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.8; DB 4; Length 18855;
 Best Local Similarity 48.3%; Pred. No. 2.3e+02;
 RESULT 1317
 Query Match 1.5%; Score 35.8; DB 13; Length 110000;
 Best Local Similarity 50.3%; Pred. No. 7.4e+02;
 RESULT 1318
 ID ADQ80254 standard; cDNA; 127145 BP.
 DE Hermansky-Pudlak syndrome associated cDNA.
 PN WO2004063709-A2.
 PD 29-JUL-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 1.5%; Score 35.8; DB 13; Length 127145;
 Best Local Similarity 56.3%; Pred. No. 8.1e+02;
 RESULT 1319
 ID ABX43735 standard; cDNA; 219 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #8900.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 1.5%; Score 35.6; DB 8; Length 219;
 Best Local Similarity 54.6%; Pred. No. 14;
 RESULT 1320
 ID ACN59359 standard; cDNA; 584 BP.
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-030-Q6-K6-E4, SEQ:14140.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 1.5%; Score 35.6; DB 13; Length 584;
 Best Local Similarity 52.7%; Pred. No. 26;
 RESULT 1321
 ID ADS56832 standard; cDNA; 2008 BP.
 DE Bacterial polynucleotide #8819.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 1.5%; Score 35.6; DB 13; Length 2008;

Best Local Similarity 49.5%; Pred. No. 60;

RESULT 1322

ID ADS47566 standard; cDNA; 2109 BP.

DE Bacterial polynucleotide #2309.

PN US2003233675-A1.

PD 18-DEC-2003.

PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

Query Match 1.5%; Score 35.6; DB 13; Length 2109;

Best Local Similarity 45.6%; Pred. No. 62;

RESULT 1323

ID AAZ93713 standard; DNA; 2112 BP..

DE F-box protein Pop2 coding sequence.

PN WO200022110-A2.

PD 20-APR-2000.

PA (HARD) HARVARD COLLEGE.

Query Match 1.5%; Score 35.6; DB 3; Length 2112;

Best Local Similarity 45.6%; Pred. No. 62;

RESULT 1324

ID AAT84152 standard; DNA; 2314 BP.

DE DNA encoding a Staphylococcus aureus protein of unknown function.

PN WO9730070-A1.

PD 21-AUG-1997.

PA (SMIK) SMITHKLINE BEECHAM CORP.

Query Match 1.5%; Score 35.6; DB 2; Length 2314;

Best Local Similarity 47.6%; Pred. No. 66;

RESULT 1325

ID ADS56393 standard; cDNA; 2856 BP.

DE Bacterial polynucleotide #8380.

PN US2003233675-A1.

PD 18-DEC-2003.

PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

Query Match 1.5%; Score 35.6; DB 13; Length 2856;

Best Local Similarity 51.2%; Pred. No. 76;

RESULT 1326

ID ABL32945 standard; DNA; 5234 BP.

DE Human immune system associated gene SEQ ID NO: 918.

PN WO200200928-A2.

PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 6; Length 5234;

Best Local Similarity 52.7%; Pred. No. 1.1e+02;

RESULT 1327

ID ABL32776 standard; DNA; 6782 BP.

DE Human immune system associated gene SEQ ID NO: 749.

PN WO200200928-A2.

PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 1.5%; Score 35.6; DB 6; Length 6782;

Best Local Similarity 51.2%; Pred. No. 1.3e+02;

RESULT 1328

ID AAX20267 standard; DNA; 6810 BP.
DE Borrelia burgdorferi polynucleotide sequence #20.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match 1.5%; Score 35.6; DB 2; Length 6810;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;

RESULT 1329

ID ABN80082 standard; DNA; 10250 BP.
DE Human chemically modified disease associated gene SEQ ID NO 99.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 6; Length 10250;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;

RESULT 1330

ID ABL92221 standard; DNA; 11049 BP.
DE Chemically treated DNA repair gene fragment complementary to#15.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 6; Length 11049;
Best Local Similarity 51.9%; Pred. No. 1.9e+02;

RESULT 1331

ID ABL49324 standard; DNA; 11049 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 24.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 6; Length 11049;
Best Local Similarity 51.9%; Pred. No. 1.9e+02;

RESULT 1332

ID AAS45501 standard; DNA; 11812 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #103.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 4; Length 11812;
Best Local Similarity 49.5%; Pred. No. 1.9e+02;

RESULT 1333

ID AAS46741 standard; DNA; 11812 BP.
DE Tumour suppressor gene derived chemically modified sequence #465.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 4; Length 11812;
Best Local Similarity 49.5%; Pred. No. 1.9e+02;

RESULT 1334

ID ABL34118 standard; DNA; 11812 BP.
DE Human immune system associated gene SEQ ID NO: 2091.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 6; Length 11812;
Best Local Similarity 49.5%; Pred. No. 1.9e+02;

RESULT 1335

ID ABK28431 standard; DNA; 11812 BP.
DE DNA transcription associated genomic DNA #153.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 6; Length 11812;
Best Local Similarity 49.5%; Pred. No. 1.9e+02;

RESULT 1336

ID ABL32571 standard; DNA; 18997 BP.
DE Human immune system associated gene SEQ ID NO: 544.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 6; Length 18997;
Best Local Similarity 49.2%; Pred. No. 2.7e+02;

RESULT 1337

ID ABK33949 standard; DNA; 18997 BP.
DE Human DNA for staging of Astrocytomas, complement, #16.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 6; Length 18997;
Best Local Similarity 49.2%; Pred. No. 2.7e+02;

RESULT 1338

ID ADA20353 standard; DNA; 18997 BP.
DE Prostate tumour related genomic DNA complement sample #9.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 8; Length 18997;
Best Local Similarity 49.2%; Pred. No. 2.7e+02;

RESULT 1339

ID ADA84160 standard; DNA; 18997 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:18.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 1.5%; Score 35.6; DB 8; Length 18997;
Best Local Similarity 49.2%; Pred. No. 2.7e+02;

RESULT 1340

Query Match 1.5%; Score 35.6; DB 2; Length 110000;
Best Local Similarity 55.7%; Pred. No. 8.5e+02;

RESULT 1341

ID ADS69964 standard; cDNA; 262 BP.
DE Corn seedling-derived polynucleotide (cpds), SEQ ID 4980.
PN US2003237110-A9.
PD 25-DEC-2003.
PA (INCY-) INCYTE PHARM INC.
Query Match 1.5%; Score 35.4; DB 7; Length 262;
Best Local Similarity 53.2%; Pred. No. 18;

RESULT 1342

ID ABN65577 standard; cDNA; 556 BP.
DE Human cancer related polynucleotide SEQ ID NO 5544.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.
 Query Match 1.5%; Score 35.4; DB 6; Length 556;
 Best Local Similarity 53.2%; Pred. No. 29;

RESULT 1343
 ID AAK88255 standard; cDNA; 612 BP.
 DE Human digestive system antigen coding sequence SEQ ID NO: 571.
 PN WO200155314-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.4; DB 4; Length 612;
 Best Local Similarity 52.9%; Pred. No. 31;

RESULT 1344
 ID AAS39407 standard; cDNA; 612 BP.
 DE cDNA encoding novel human colon associated polypeptide #60.
 PN WO200155302-A2.
 PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.4; DB 5; Length 612;
 Best Local Similarity 52.9%; Pred. No. 31;

RESULT 1345
 ID ADB32133 standard; cDNA; 612 BP.
 DE Human novel colon related polypeptide cDNA SEQ ID NO 70.
 PN US2003050231-A1.
 PD 13-MAR-2003.

PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 1.5%; Score 35.4; DB 9; Length 612;
 Best Local Similarity 52.9%; Pred. No. 31;

RESULT 1346
 ID AAH34792 standard; cDNA; 707 BP.
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:1874.
 PN WO200122920-A2.
 PD 05-APR-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.4; DB 4; Length 707;
 Best Local Similarity 49.7%; Pred. No. 34;

RESULT 1347
 ID ADJ43568 standard; cDNA; 824 BP.
 DE Plant cDNA #4568.
 PN US2004016025-A1.
 PD 22-JAN-2004.

PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZE BROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 PA (ZHUT/) ZHU T.
 Query Match 1.5%; Score 35.4; DB 12; Length 824;
 Best Local Similarity 53.2%; Pred. No. 38;

RESULT 1348
 ID ADB52352 standard; DNA; 864 BP.

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:2894.
 PN WO2003065993-A2.
 PD 14-AUG-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 1.5%; Score 35.4; DB 10; Length 864;
 Best Local Similarity 52.3%; Pred. No. 39;
 RESULT 1349
 ID ABK73608 standard; DNA; 1140 BP.
 DE Bacillus licheniformis genomic sequence tag (GST) #899.
 PN WO200229113-A2.
 PD 11-APR-2002.
 PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES AS.
 Query Match 1.5%; Score 35.4; DB 6; Length 1140;
 Best Local Similarity 47.5%; Pred. No. 47;
 RESULT 1350
 ID AAC36917 standard; DNA; 1203 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15522.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.5%; Score 35.4; DB 3; Length 1203;
 Best Local Similarity 54.1%; Pred. No. 49;
 RESULT 1351
 ID ABD16646 standard; DNA; 1272 BP.
 DE Pseudomonas aeruginosa polynucleotide #15250.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.5%; Score 35.4; DB 11; Length 1272;
 Best Local Similarity 52.3%; Pred. No. 51;
 RESULT 1352
 ID ABZ13055 standard; DNA; 1455 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 860.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.5%; Score 35.4; DB 6; Length 1455;
 Best Local Similarity 52.3%; Pred. No. 56;
 RESULT 1353
 ID ADC25954 standard; DNA; 1455 BP.
 DE Thale cress UDP-glucosyltransferase DNA.
 PN WO2003066836-A2.
 PD 14-AUG-2003.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 1.5%; Score 35.4; DB 10; Length 1455;
 Best Local Similarity 52.3%; Pred. No. 56;
 RESULT 1354
 ID AAD13657 standard; DNA; 1473 BP.
 DE Arabidopsis thaliana glucosyltransferase (GTase) A41 gene.
 PN WO200159140-A1.
 PD 16-AUG-2001.
 PA (UYYO-) UNIV YORK.
 Query Match 1.5%; Score 35.4; DB 4; Length 1473;
 Best Local Similarity 52.3%; Pred. No. 56;
 RESULT 1355
 ID ADJ40246 standard; cDNA; 1479 BP.

DE Plant cDNA #1246.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZE BROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 PA (ZHUT/) ZHU T.
 Query Match 1.5%; Score 35.4; DB 12; Length 1479;
 Best Local Similarity 53.2%; Pred. No. 56;
 RESULT 1356
 ID ADA71336 standard; DNA; 1490 BP.
 DE Rice gene, SEQ ID 4659.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.5%; Score 35.4; DB 8; Length 1490;
 Best Local Similarity 45.7%; Pred. No. 56;
 RESULT 1357
 ID AAC42466 standard; DNA; 1516 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35666.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.5%; Score 35.4; DB 3; Length 1516;
 Best Local Similarity 52.3%; Pred. No. 57;
 RESULT 1358
 ID ABD16834 standard; DNA; 1614 BP.
 DE Pseudomonas aeruginosa polynucleotide #15438.
 PN US6551795-B1.
 PD 22-APR-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.5%; Score 35.4; DB 11; Length 1614;
 Best Local Similarity 52.3%; Pred. No. 60;
 RESULT 1359
 ID AAC47594 standard; DNA; 1669 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54396.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.5%; Score 35.4; DB 3; Length 1669;
 Best Local Similarity 54.1%; Pred. No. 61;
 RESULT 1360
 ID ABA99470 standard; cDNA; 1715 BP.
 DE B. napus SGT1 cDNA.
 PN WO200206320-A2.
 PD 24-JAN-2002.
 PA (PFLA-) INST PFLANZENBIOCHEMIE.
 Query Match 1.5%; Score 35.4; DB 6; Length 1715;
 Best Local Similarity 52.3%; Pred. No. 62;
 RESULT 1361
 ID AAC47078 standard; DNA; 1759 BP.
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52482.

PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 1.5%; Score 35.4; DB 3; Length 1759;
 Best Local Similarity 54.1%; Pred. No. 63;
 RESULT 1362
 ID ADA71684 standard; DNA; 2000 BP.
 DE Rice gene, SEQ ID 5009.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.5%; Score 35.4; DB 8; Length 2000;
 Best Local Similarity 48.7%; Pred. No. 69;
 RESULT 1363
 ID ADO36063 standard; DNA; 2902 BP.
 DE Novel mouse gene sequence #736.
 PN WO2004046310-A2.
 PD 03-JUN-2004.
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 Query Match 1.5%; Score 35.4; DB 12; Length 2902;
 Best Local Similarity 56.4%; Pred. No. 88;
 RESULT 1364
 ID ABL08782 standard; cDNA; 5059 BP.
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 20828.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.5%; Score 35.4; DB 4; Length 5059;
 Best Local Similarity 46.5%; Pred. No. 1.3e+02;
 RESULT 1365
 ID AAS46721 standard; DNA; 5995 BP.
 DE Tumour suppressor gene derived chemically modified sequence #444.
 PN WO200168912-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.4; DB 4; Length 5995;
 Best Local Similarity 48.7%; Pred. No. 1.4e+02;
 RESULT 1366
 ID AAX13432 standard; DNA; 6645 BP.
 DE Enterococcus faecalis genome contig SEQ ID NO:495.
 PN WO9850555-A2.
 PD 12-NOV-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.4; DB 2; Length 6645;
 Best Local Similarity 49.2%; Pred. No. 1.5e+02;
 RESULT 1367
 ID ABS99227 standard; DNA; 6645 BP.
 DE Enterococcus faecalis contig sequence #495.
 PN US2002120116-A1.
 PD 29-AUG-2002.
 PA (KUNS/) KUNSCH C A.
 PA (DILL/) DILLON P J.
 PA (BARA/) BARASH S.
 Query Match 1.5%; Score 35.4; DB 6; Length 6645;
 Best Local Similarity 49.2%; Pred. No. 1.5e+02;
 RESULT 1368
 ID ABL33929 standard; DNA; 6801 BP.
 DE Human immune system associated gene SEQ ID NO: 1902.

PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.4; DB 6; Length 6801;
 Best Local Similarity 46.8%; Pred. No. 1.5e+02;
 RESULT 1369
 ID ABL92291 standard; DNA; 6801 BP.
 DE Chemically treated DNA repair gene fragment complementary to#50.
 PN WO200181622-A2.
 PD 01-NOV-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.4; DB 6; Length 6801;
 Best Local Similarity 46.8%; Pred. No. 1.5e+02;
 RESULT 1370
 ID ABL49362 standard; DNA; 6801 BP.
 DE Human polynucleotide associated with DNA replication SEQ ID NO 62.
 PN WO200177377-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.4; DB 6; Length 6801;
 Best Local Similarity 46.8%; Pred. No. 1.5e+02;
 RESULT 1371
 ID ABL33637 standard; DNA; 7306 BP.
 DE Human immune system associated gene SEQ ID NO: 1610.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.4; DB 6; Length 7306;
 Best Local Similarity 45.5%; Pred. No. 1.6e+02;
 RESULT 1372
 ID AAI99335 standard; DNA; 7408 BP.
 DE Human excretory related polynucleotide SEQ ID NO 1099.
 PN WO200155313-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.4; DB 4; Length 7408;
 Best Local Similarity 55.2%; Pred. No. 1.6e+02;
 RESULT 1373
 ID AAI63685 standard; DNA; 7408 BP.
 DE Human kidney related polynucleotide SEQ ID NO 1000.
 PN WO200155323-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.4; DB 5; Length 7408;
 Best Local Similarity 55.2%; Pred. No. 1.6e+02;
 RESULT 1374
 ID ABK31382 standard; DNA; 7459 BP.
 DE Signal transduction associated gene modified DNA #113.
 PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.4; DB 6; Length 7459;
 Best Local Similarity 46.0%; Pred. No. 1.6e+02;
 RESULT 1375
 ID ABL92304 standard; DNA; 13919 BP.
 DE Chemically treated DNA repair gene fragment#57.
 PN WO200181622-A2.

PD 01-NOV-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.4; DB 6; Length 13919;
 Best Local Similarity 51.6%; Pred. No. 2.5e+02;
 RESULT 1376
 ID ABL32654 standard; DNA; 17211 BP.
 DE Human immune system associated gene SEQ ID NO: 627.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.4; DB 6; Length 17211;
 Best Local Similarity 49.2%; Pred. No. 2.9e+02;
 RESULT 1377
 ID AAK67051 standard; DNA; 30626 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21863.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35.4; DB 4; Length 30626;
 Best Local Similarity 49.2%; Pred. No. 4.2e+02;
 RESULT 1378
 ID ACN45192 standard; DNA; 82660 BP.
 DE Mouse genomic sequence mCG9397.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.5%; Score 35.4; DB 11; Length 82660;
 Best Local Similarity 55.2%; Pred. No. 8.1e+02;
 RESULT 1379
 ID ADB12769 standard; DNA; 139308 BP.
 DE Human PRKR DNA.
 PN DE10128838-A1.
 PD 02-JAN-2003.
 PA (GENP-) GENPROFILE AG.
 Query Match 1.5%; Score 35.4; DB 8; Length 139308;
 Best Local Similarity 55.2%; Pred. No. 1.1e+03;
 RESULT 1380
 ID AAC10087 standard; cDNA; 274 BP.
 DE Human secreted protein 5' EST, SEQ ID NO: 14162.
 PN EP1033401-A2.
 PD 06-SEP-2000.
 PA (GEST) GENSET.
 Query Match 1.5%; Score 35.2; DB 3; Length 274;
 Best Local Similarity 59.8%; Pred. No. 21;
 RESULT 1381
 ID ADL43834 standard; DNA; 461 BP.
 DE Human ovarian cancer DNA marker #17724.
 PN WO200170979-A2.
 PD 27-SEP-2001.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 Query Match 1.5%; Score 35.2; DB 5; Length 461;
 Best Local Similarity 51.4%; Pred. No. 30;
 RESULT 1382
 ID ACH78507 standard; DNA; 507 BP.
 DE Human genome derived single exon probe #11702.
 PN US2003194704-A1.
 PD 16-OCT-2003.

PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.

Query Match 1.5%; Score 35.2; DB 12; Length 507;
Best Local Similarity 52.8%; Pred. No. 32;

RESULT 1383

ID ADR60605 standard; cDNA; 639 BP.
DE Cotton cDNA sequence, SEQ ID 1386.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.

Query Match 1.5%; Score 35.2; DB 13; Length 639;
Best Local Similarity 52.0%; Pred. No. 37;

RESULT 1384

ID ABN69110 standard; DNA; 786 BP.
DE Streptococcus polynucleotide SEQ ID NO 6133.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.

Query Match 1.5%; Score 35.2; DB 6; Length 786;
Best Local Similarity 52.8%; Pred. No. 42;

RESULT 1385

ID ABN98454 standard; DNA; 1011 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 222.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYU/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.

Query Match 1.5%; Score 35.2; DB 6; Length 1011;
Best Local Similarity 50.3%; Pred. No. 50;

RESULT 1386

ID ACH92210 standard; DNA; 1101 BP.
DE Human genome derived single exon probe #25405.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

Query Match 1.5%; Score 35.2; DB 12; Length 1101;

Best Local Similarity 52.8%; Pred. No. 53;

RESULT 1387

ID ABZ42066 standard; cDNA; 1473 BP.

DE Arabidopsis thaliana gene #50 modulated by PTGS.

PN WO200281695-A2.

PD 17-OCT-2002.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PA (FRIE-) FRIEDRICH MIESCHER INST.

Query Match 1.5%; Score 35.2; DB 8; Length 1473;

Best Local Similarity 48.5%; Pred. No. 64;

RESULT 1388

ID AAV16721 standard; cDNA to mRNA; 1506 BP.

DE Nucleic acid encoding rat Neural-Wiskott-Aldrich syndrome protein.

PN JP10072494-A.

PD 17-MAR-1998.

PA (MITS-) MITSUI SEIYAKU KOGYO KK.

PA (TAKE/) TAKENAWA T.

Query Match 1.5%; Score 35.2; DB 2; Length 1506;

Best Local Similarity 52.0%; Pred. No. 65;

RESULT 1389

ID AAH77907 standard; DNA; 1588 BP.

DE Nucleotide sequence of a rat N-WASP protein.

PN WO200144292-A2.

PD 21-JUN-2001.

PA (CNRS) CENT NAT RECH SCI.

PA (CURI-) INST CURIE.

Query Match 1.5%; Score 35.2; DB 4; Length 1588;

Best Local Similarity 52.0%; Pred. No. 68;

RESULT 1390

ID ABZ16116 standard; DNA; 2000 BP.

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 3921.

PN WO200216655-A2.

PD 28-FEB-2002.

PA (SCRI) SCRIPPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.5%; Score 35.2; DB 6; Length 2000;

Best Local Similarity 49.0%; Pred. No. 79;

RESULT 1391

ID ABT42528 standard; DNA; 2049 BP.

DE Human nucleic acid-associated protein (NAAP) coding sequence #9.

PN WO2003010329-A2.

PD 06-FEB-2003.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 1.5%; Score 35.2; DB 8; Length 2049; ..

Best Local Similarity 52.8%; Pred. No. 80;

RESULT 1392

ID ADC30266 standard; cDNA; 2069 BP.

DE Human novel cDNA sequence, SEQ ID NO:348.

PN WO2003029271-A2.

PD 10-APR-2003.

PA (HYSE-) HYSEQ INC.

Query Match 1.5%; Score 35.2; DB 10; Length 2069;

Best Local Similarity 52.8%; Pred. No. 81;

RESULT 1393

ID ADF03150 standard; DNA; 2208 BP.

DE Bacterial polynucleotide #3435.
 PN US6605709-B1.
 PD 12-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.5%; Score 35.2; DB 10; Length 2208;
 Best Local Similarity 49.0%; Pred. No. 84;
 RESULT 1394
 ID ADM02604 standard; cDNA; 2241 BP.
 DE Human cDNA of the invention SEQ ID NO:1289.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 1.5%; Score 35.2; DB 11; Length 2241;
 Best Local Similarity 52.8%; Pred. No. 85;
 RESULT 1395
 ID ADM02673 standard; cDNA; 2525 BP.
 DE Human cDNA of the invention SEQ ID NO:1358.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 1.5%; Score 35.2; DB 11; Length 2525;
 Best Local Similarity 52.8%; Pred. No. 92;
 RESULT 1396
 ID ABZ32269 standard; DNA; 2625 BP.
 DE Candida albicans essential gene SEQ ID NO 6556.
 PN WO200253728-A2.
 PD 11-JUL-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 1.5%; Score 35.2; DB 6; Length 2625;
 Best Local Similarity 52.0%; Pred. No. 94;
 RESULT 1397
 ID ADS89352 standard; DNA; 3862 BP.
 DE Oligonucleotide of the invention SEQ ID NO:368.
 PN WO2004035803-A2.
 PD 29-APR-2004.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 13; Length 3862;
 Best Local Similarity 49.0%; Pred. No. 1.2e+02;
 RESULT 1398
 ID ABK40013 standard; DNA; 5244 BP.
 DE Human chemically pretreated gene sequence #48 strand 1.
 PN WO200202806-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 5244;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 RESULT 1399
 ID ABL32828 standard; DNA; 6009 BP.
 DE Human immune system associated gene SEQ ID NO: 801.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6009;
 Best Local Similarity 52.0%; Pred. No. 1.6e+02;
 RESULT 1400
 ID ABK31371 standard; DNA; 6012 BP.
 DE Signal transduction associated gene modified complementary DNA #107.

PN WO200200926-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6012;
 Best Local Similarity 48.5%; Pred. No. 1.6e+02;
 RESULT 1401
 ID ABL70328 standard; DNA; 6012 BP.
 DE Chemically treated cell signalling DNA sequence complementary to#109.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6012;
 Best Local Similarity 48.5%; Pred. No. 1.6e+02;
 RESULT 1402
 ID AAS61275 standard; DNA; 6012 BP.
 DE Human gene regulation-associated gene oligonucleotide #230.
 PN WO200177375-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6012;
 Best Local Similarity 48.5%; Pred. No. 1.6e+02;
 RESULT 1403
 ID AAS46300 standard; DNA; 6862 BP.
 DE Tumour suppressor gene derived chemically modified sequence #22.
 PN WO200168912-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 4; Length 6862;
 Best Local Similarity 49.0%; Pred. No. 1.8e+02;
 RESULT 1404
 ID ABL32223 standard; DNA; 6862 BP.
 DE Human immune system associated gene SEQ ID NO: 196.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6862;
 Best Local Similarity 49.0%; Pred. No. 1.8e+02;
 RESULT 1405
 ID AAS61082 standard; DNA; 6862 BP.
 DE Human gene regulation-associated gene oligonucleotide #37.
 PN WO200177375-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 6862;
 Best Local Similarity 49.0%; Pred. No. 1.8e+02;
 RESULT 1406
 ID ABN80083 standard; DNA; 10250 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 100.
 PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 10250;
 Best Local Similarity 52.0%; Pred. No. 2.3e+02;
 RESULT 1407
 ID ABL34179 standard; DNA; 13084 BP.
 DE Human immune system associated gene SEQ ID NO: 2152.
 PN WO200200928-A2.

PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 13084;
 Best Local Similarity 54.7%; Pred. No. 2.7e+02;
 RESULT 1408
 ID ABL33344 standard; DNA; 17674 BP.
 DE Human immune system associated gene SEQ ID NO: 1317.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35.2; DB 6; Length 17674;
 Best Local Similarity 52.0%; Pred. No. 3.3e+02;
 RESULT 1409
 ID ADA02885 standard; DNA; 96593 BP.
 DE Mouse Blm carcinoma associated gene, SEQ ID NO:1403.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.5%; Score 35.2; DB 9; Length 96593;
 Best Local Similarity 53.7%; Pred. No. 1e+03;
 RESULT 1410
 ID ADB72623 standard; DNA; 96593 BP.
 DE Mouse Blm gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.5%; Score 35.2; DB 10; Length 96593;
 Best Local Similarity 53.7%; Pred. No. 1e+03;
 RESULT 1411
 ID ADM74480 standard; DNA; 96593 BP.
 DE Murine carcinoma associated (CA) nucleic acid #76.
 PN US2004072154-A1.
 PD 15-APR-2004.
 PA (MORR/) MORRIS D W.
 PA (ENGE/) ENGELHARD E K.
 Query Match 1.5%; Score 35.2; DB 12; Length 96593;
 Best Local Similarity 53.7%; Pred. No. 1e+03;
 RESULT 1412
 ID ADC85364 standard; DNA; 96594 BP.
 DE Human Pap coding sequence.
 PN WO2003045230-A2.
 PD 05-JUN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.5%; Score 35.2; DB 10; Length 96594;
 Best Local Similarity 53.7%; Pred. No. 1e+03;
 RESULT 1413
 ID ACN43994 standard; DNA; 109586 BP.
 DE Human genomic sequence hCG23847.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.5%; Score 35.2; DB 11; Length 109586;
 Best Local Similarity 45.8%; Pred. No. 1.1e+03;
 RESULT 1414
 ID AAT42063 standard; DNA; 1830121 BP.
 DE Haemophilus influenzae complete genome sequence.
 PN WO9633276-A1.

PD 24-OCT-1996.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (UYJO) UNIV JOHNS HOPKINS.
 Query Match 1.5%; Score 35.2; DB 2; Length 110000;
 Best Local Similarity 47.0%; Pred. No. 1.1e+03;
 RESULT 1415
 Query Match 1.5%; Score 35.2; DB 5; Length 110000;
 Best Local Similarity 50.9%; Pred. No. 1.1e+03;
 RESULT 1416
 Query Match 1.5%; Score 35.2; DB 6; Length 110000;
 Best Local Similarity 52.8%; Pred. No. 1.1e+03;
 RESULT 1417
 ID ABD32827 standard; DNA; 129381 BP.
 DE Human cancer-associated genomic DNA HD17-008.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.5%; Score 35.2; DB 13; Length 129381;
 Best Local Similarity 50.6%; Pred. No. 1.2e+03;
 RESULT 1418
 ID AAK74668 standard; DNA; 340 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29480.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35; DB 4; Length 340;
 Best Local Similarity 49.2%; Pred. No. 28;
 RESULT 1419
 ID AAK74669 standard; DNA; 340 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29481.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 1.5%; Score 35; DB 4; Length 340;
 Best Local Similarity 49.2%; Pred. No. 28;
 RESULT 1420
 ID AAF62609 standard; DNA; 1413 BP.
 DE R. serpentina arbutin synthase DNA.
 PN WO200107631-A2.
 PD 01-FEB-2001.
 PA (HENK) HENKEL KGAA.
 Query Match 1.5%; Score 35; DB 4; Length 1413;
 Best Local Similarity 54.2%; Pred. No. 72;
 RESULT 1421
 ID AAD13665 standard; DNA; 1425 BP.
 DE Arabidopsis thaliana glucosyltransferase (GTase). A962 gene.
 PN WO200159140-A1.
 PD 16-AUG-2001.
 PA (UYYO-) UNIV YORK.
 Query Match 1.5%; Score 35; DB 4; Length 1425;
 Best Local Similarity 52.4%; Pred. No. 72;
 RESULT 1422
 ID ABZ14807 standard; DNA; 1425 BP.
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2612.
 PN WO200216655-A2.
 PD 28-FEB-2002.
 PA (SCRI) SCRIPPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.5%; Score 35; DB 6; Length 1425;
 Best Local Similarity 52.4%; Pred. No. 72;
 RESULT 1423
 ID ADA70022 standard; DNA; 1485 BP.
 DE Rice gene, SEQ ID 3345.
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match 1.5%; Score 35; DB 8; Length 1485;
 Best Local Similarity 50.9%; Pred. No. 74;
 RESULT 1424
 ID ADJ39593 standard; cDNA; 1485 BP.
 DE Plant cDNA #593.
 PN US2004016025-A1.
 PD 22-JAN-2004.
 PA (BUDW/) BUDWORTH P.
 PA (MOUG/) MOUGHAMER T.
 PA (BRIG/) BRIGGS S P.
 PA (COOP/) COOPER B.
 PA (GLAZ/) GLAZE BROOK J.
 PA (GOFF/) GOFF S A.
 PA (KATA/) KATAGIRI F.
 PA (KREP/) KREPS J.
 PA (PROV/) PROVART N.
 PA (RICK/) RICKE D.
 PA (ZHUT/) ZHU T.
 Query Match 1.5%; Score 35; DB 12; Length 1485;
 Best Local Similarity 50.9%; Pred. No. 74;
 RESULT 1425
 ID ACA22042 standard; DNA; 3277 BP.
 DE Prokaryotic essential gene #3699.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 1.5%; Score 35; DB 8; Length 3277;
 Best Local Similarity 59.6%; Pred. No. 1.3e+02;
 RESULT 1426
 ID ACA21975 standard; DNA; 4217 BP.
 DE Prokaryotic essential gene #3632.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 1.5%; Score 35; DB 8; Length 4217;
 Best Local Similarity 59.6%; Pred. No. 1.5e+02;
 RESULT 1427
 ID ABL33906 standard; DNA; 4415 BP.
 DE Human immune system associated gene SEQ ID NO: 1879.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35; DB 6; Length 4415;
 Best Local Similarity 47.9%; Pred. No. 1.5e+02;
 RESULT 1428
 ID ABL34602 standard; DNA; 4415 BP.
 DE Human metastasis associated gene SEQ ID NO: 155.
 PN WO200177376-A2.

PD 18-OCT-2001.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35; DB 6; Length 4415;
 Best Local Similarity 47.9%; Pred. No. 1.5e+02;
 RESULT 1429
 ID ABL70423 standard; DNA; 4415 BP.
 DE Chemically treated cell signalling DNA sequence#157.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIC-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35; DB 6; Length 4415;
 Best Local Similarity 47.9%; Pred. No. 1.5e+02;
 RESULT 1430
 ID ADS99863 standard; DNA; 4415 BP.
 DE Bisulphite treated human gene associated with metastasis #78.
 PN US2003148327-A1.
 PD 07-AUG-2003.
 PA (OLEK/) OLEK A.
 PA (PIEP/) PIEPENBROCK C.
 PA (BERL/) BERLIN K.
 Query Match 1.5%; Score 35; DB 7; Length 4415;
 Best Local Similarity 47.9%; Pred. No. 1.5e+02;
 RESULT 1431
 ID ADS48728 standard; cDNA; 4566 BP.
 DE Bacterial polynucleotide #3471.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 1.5%; Score 35; DB 13; Length 4566;
 Best Local Similarity 50.3%; Pred. No. 1.6e+02;
 RESULT 1432
 ID ADQ23570 standard; DNA; 4944 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6390.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 1.5%; Score 35; DB 12; Length 4944;
 Best Local Similarity 55.3%; Pred. No. 1.6e+02;
 RESULT 1433
 ID AAQ80911 standard; cDNA; 5181 BP.
 DE Plasmodium falciparum MSA-1 gene cDNA.
 PN WO9428930-A1.
 PD 22-DEC-1994.
 PA (VIRO-) VIROGENETICS CORP.
 Query Match 1.5%; Score 35; DB 2; Length 5181;
 Best Local Similarity 55.3%; Pred. No. 1.7e+02;
 RESULT 1434
 ID ABD32852 standard; cDNA; 5895 BP.
 DE Mouse cancer-associated cDNA MR17-032.1.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.5%; Score 35; DB 13; Length 5895;

Best Local Similarity 51.6%; Pred. No. 1.9e+02;
 RESULT 1435
 ID ADP76048 standard; DNA; 5935 BP.
 DE DNA of mouse epidermal growth factor receptor, SEQ ID No 23.
 PN WO2004055055-A1.
 PD 01-JUL-2004.
 PA (LICN) LICENTIA LTD.
 Query Match 1.5%; Score 35; DB 13; Length 5935;
 Best Local Similarity 51.6%; Pred. No. 1.9e+02;
 RESULT 1436
 ID AAA81730 standard; DNA; 9133 BP.
 DE N. meningitidis partial DNA sequence gnm_277 SEQ ID NO:277.
 PN WO200022430-A2.
 PD 20-APR-2000.
 PA (CHIR) CHIRON CORP.
 Query Match 1.5%; Score 35; DB 3; Length 9133;
 Best Local Similarity 55.3%; Pred. No. 2.5e+02;
 RESULT 1437
 ID ABL70189 standard; DNA; 15282 BP.
 DE Chemically treated cell signalling DNA sequence#40.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35; DB 6; Length 15282;
 Best Local Similarity 49.7%; Pred. No. 3.5e+02;
 RESULT 1438
 ID AAS61139 standard; DNA; 15282 BP.
 DE Human gene regulation-associated gene oligonucleotide #94.
 PN WO200177375-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35; DB 6; Length 15282;
 Best Local Similarity 49.7%; Pred. No. 3.5e+02;
 RESULT 1439
 ID ABL33415 standard; DNA; 17389 BP.
 DE Human immune system associated gene SEQ ID NO: 1388.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 35; DB 6; Length 17389;
 Best Local Similarity 49.7%; Pred. No. 3.8e+02;
 RESULT 1440
 ID ACN43954 standard; DNA; 95683 BP.
 DE Human genomic sequence hCG37570.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.5%; Score 35; DB 11; Length 95683;
 Best Local Similarity 53.2%; Pred. No. 1.2e+03;
 RESULT 1441
 Query Match 1.5%; Score 35; DB 3; Length 110000;
 Best Local Similarity 55.3%; Pred. No. 1.3e+03;
 RESULT 1442
 Query Match 1.5%; Score 35; DB 12; Length 110000;
 Best Local Similarity 47.5%; Pred. No. 1.3e+03;
 RESULT 1443
 ID ADQ97319 standard; DNA; 117829 BP.

DE Human cancer associated sequence HD08-031, SEQ ID 296.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.5%; Score 35; DB 12; Length 117829;
 Best Local Similarity 45.7%; Pred. No. 1.3e+03;
 RESULT 1444
 ID ABQ88126 standard; cDNA; 159400 BP.
 DE Human osteoblast differentiation related cDNA SEQ ID NO 33.
 PN WO200250301-A2.
 PD 27-JUN-2002.
 PA (GENE-) GENE LOGIC INC.
 PA (PROC) PROCTER & GAMBLE CO.
 Query Match 1.5%; Score 35; DB 6; Length 159400;
 Best Local Similarity 53.2%; Pred. No. 1.6e+03;
 RESULT 1445
 ID ABD32851 standard; DNA; 181413 BP.
 DE Mouse cancer-associated genomic DNA MD17-032.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.5%; Score 35; DB 13; Length 181413;
 Best Local Similarity 51.6%; Pred. No. 1.8e+03;
 RESULT 1446
 ID AAF21608 standard; DNA; 349980 BP.
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
 PN WO200066791-A1.
 PD 09-NOV-2000.
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 Query Match 1.5%; Score 35; DB 3; Length 349980;
 Best Local Similarity 55.3%; Pred. No. 2.6e+03;
 RESULT 1447
 ID ABX38043 standard; cDNA; 413 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #3208.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 1.5%; Score 34.8; DB 8; Length 413;
 Best Local Similarity 52.8%; Pred. No. 36;
 RESULT 1448
 ID ACN49798 standard; cDNA; 495 BP.
 DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-N6-A10, SEQ:4579.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 1.5%; Score 34.8; DB 13; Length 495;
 Best Local Similarity 50.6%; Pred. No. 41;
 RESULT 1449
 ID ACA05131 standard; cDNA; 531 BP.
 DE Rice leaf expression sequence label #44.

PN CN1367260-A.
PD 04-SEP-2002.
PA (UYZH-) UNIV ZHEJIANG.

Query Match 1.5%; Score 34.8; DB 8; Length 531;
Best Local Similarity 60.6%; Pred. No. 43;

RESULT 1450

ID ADJ43307 standard; cDNA; 615 BP.
DE Plant cDNA #4307.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZE BROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.

Query Match 1.5%; Score 34.8; DB 12; Length 615;
Best Local Similarity 52.8%; Pred. No. 47;

RESULT 1451

ID ADK59885 standard; DNA; 624 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #7268.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.

Query Match 1.5%; Score 34.8; DB 10; Length 624;
Best Local Similarity 56.8%; Pred. No. 48;

RESULT 1452

ID ABZ12278 standard; DNA; 1158 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 83.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Query Match 1.5%; Score 34.8; DB 6; Length 1158;
Best Local Similarity 51.3%; Pred. No. 72;

RESULT 1453

ID ABL29557 standard; DNA; 1200 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 40144.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

Query Match 1.5%; Score 34.8; DB 4; Length 1200;
Best Local Similarity 55.9%; Pred. No. 74;

RESULT 1454

ID ABZ66714 standard; DNA; 1329 BP.
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 90.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.

Query Match 1.5%; Score 34.8; DB 10; Length 1329;
Best Local Similarity 50.6%; Pred. No. 79;

RESULT 1455

ID ACA29043 standard; DNA; 1386 BP.
DE Prokaryotic essential gene #10700.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.5%; Score 34.8; DB 8; Length 1386;
Best Local Similarity 45.3%; Pred. No. 81;

RESULT 1456

ID ADF89822 standard; DNA; 1726 BP.
DE Triterpene saponin pathway associated nucleotide sequence, SEQ ID 30.
PN WO2003093425-A2.
PD 13-NOV-2003.
PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.
Query Match 1.5%; Score 34.8; DB 10; Length 1726;
Best Local Similarity 45.3%; Pred. No. 94;

RESULT 1457

ID ACA31023 standard; DNA; 2001 BP.
DE Prokaryotic essential gene #12680.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 1.5%; Score 34.8; DB 8; Length 2001;
Best Local Similarity 50.6%; Pred. No. 1e+02;

RESULT 1458

ID ABL30171 standard; DNA; 2350 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41986.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 1.5%; Score 34.8; DB 4; Length 2350;
Best Local Similarity 52.0%; Pred. No. 1.2e+02;

RESULT 1459

ID ABN84912 standard; cDNA; 2846 BP.
DE AMP-binding enzyme family 33217 cDNA.
PN WO200259284-A2.
PD 01-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 34.8; DB 6; Length 2846;
Best Local Similarity 31.5%; Pred. No. 1.3e+02;

RESULT 1460

ID ADL14183 standard; cDNA; 2846 BP.
DE Novel human gene 33217 cDNA.
PN US2004058355-A1.
PD 25-MAR-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 1.5%; Score 34.8; DB 12; Length 2846;
Best Local Similarity 31.5%; Pred. No. 1.3e+02;

RESULT 1461

ID ABD32853 standard; cDNA; 2986 BP.
DE Mouse cancer-associated cDNA MR17-032.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 1.5%; Score 34.8; DB 13; Length 2986;
Best Local Similarity 48.9%; Pred. No. 1.4e+02;

RESULT 1462

ID ABL29556 standard; DNA; 3323 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 40141.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.5%; Score 34.8; DB 4; Length 3323;
 Best Local Similarity 55.9%; Pred. No. 1.5e+02;
 RESULT 1463
 ID ABL50557 standard; DNA; 3446 BP.
 DE Micromonospora carbonacea everninomicin locus nucleotide contig 3.
 PN WO200155180-A2.
 PD 02-AUG-2001.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 PA (FARN/) FARNET C.
 Query Match 1.5%; Score 34.8; DB 4; Length 3446;
 Best Local Similarity 50.6%; Pred. No. 1.5e+02;
 RESULT 1464
 ID ABL26186 standard; DNA; 3957 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 30031.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.5%; Score 34.8; DB 4; Length 3957;
 Best Local Similarity 52.0%; Pred. No. 1.6e+02;
 RESULT 1465
 ID AAT86702 standard; DNA; 6263 BP.
 DE DNA encoding thermostable esterase E009.
 PN WO9725058-A1.
 PD 17-JUL-1997.
 PA (THER-) THERMOGEN INC.
 Query Match 1.5%; Score 34.8; DB 2; Length 6263;
 Best Local Similarity 50.6%; Pred. No. 2.2e+02;
 RESULT 1466
 ID AAS03396 standard; DNA; 6263 BP.
 DE Thermus DNA encoding a partial thermostable esterase, E009.
 PN US6218163-B1.
 PD 17-APR-2001.
 PA (THER-) THERMOGEN INC.
 Query Match 1.5%; Score 34.8; DB 4; Length 6263;
 Best Local Similarity 50.6%; Pred. No. 2.2e+02;
 RESULT 1467
 ID AAX08523 standard; DNA; 6265 BP.
 DE NBP46 (root lectin) genomic DNA.
 PN WO9907223-A1.
 PD 18-FEB-1999.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 1.5%; Score 34.8; DB 2; Length 6265;
 Best Local Similarity 47.7%; Pred. No. 2.2e+02;
 RESULT 1468
 ID AAS46760 standard; DNA; 7900 BP.
 DE Tumour suppressor gene derived chemically modified sequence #484.
 PN WO200168912-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 4; Length 7900;
 Best Local Similarity 45.6%; Pred. No. 2.6e+02;
 RESULT 1469

ID ABL19298 standard; DNA; 8005 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9367.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.5%; Score 34.8; DB 4; Length 8005;
 Best Local Similarity 55.9%; Pred. No. 2.6e+02;
 RESULT 1470
 ID ABK39954 standard; DNA; 8076 BP.
 DE Human chemically pretreated gene sequence #18 strand 1.
 PN WO200202806-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 8076;
 Best Local Similarity 48.9%; Pred. No. 2.6e+02;
 RESULT 1471
 ID ABL30170 standard; DNA; 9716 BP.
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41983.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 1.5%; Score 34.8; DB 4; Length 9716;
 Best Local Similarity 52.0%; Pred. No. 3e+02;
 RESULT 1472
 ID ABL33467 standard; DNA; 10606 BP.
 DE Human immune system associated gene SEQ ID NO: 1440.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 10606;
 Best Local Similarity 52.0%; Pred. No. 3.1e+02;
 RESULT 1473
 ID AAS45314 standard; DNA; 11260 BP.
 DE Chemically pretreated genomic DNA associated with cell cycle #10.
 PN WO200168911-A2.
 PD 20-SEP-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 4; Length 11260;
 Best Local Similarity 49.5%; Pred. No. 3.3e+02;
 RESULT 1474
 ID ABK28153 standard; DNA; 11260 BP.
 DE DNA transcription associated genomic DNA #14.
 PN WO200192565-A2.
 PD 06-DEC-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 11260;
 Best Local Similarity 49.5%; Pred. No. 3.3e+02;
 RESULT 1475
 ID ABN80038 standard; DNA; 11260 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 55.
 PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 11260;
 Best Local Similarity 49.5%; Pred. No. 3.3e+02;
 RESULT 1476
 ID AAA96368 standard; DNA; 12117 BP.

DE Polymorphic repeat microsatellite sequences present in the CTLA4 locus.
 PN WO200056856-A2.
 PD 28-SEP-2000.
 PA (GEMY) GENETICS INST INC.
 Query Match 1.5%; Score 34.8; DB 3; Length 12117;
 Best Local Similarity 57.3%; Pred. No. 3.4e+02;
 RESULT 1477
 ID ABL32729 standard; DNA; 14307 BP.
 DE Human immune system associated gene SEQ ID NO: 702.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 14307;
 Best Local Similarity 50.0%; Pred. No. 3.8e+02;
 RESULT 1478
 ID ABL32631 standard; DNA; 14987 BP.
 DE Human immune system associated gene SEQ ID NO: 604.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 14987;
 Best Local Similarity 44.3%; Pred. No. 3.9e+02;
 RESULT 1479
 ID ABN80238 standard; DNA; 15121 BP.
 DE Human chemically modified disease associated gene SEQ ID NO 255.
 PN WO200200927-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 15121;
 Best Local Similarity 47.0%; Pred. No. 4e+02;
 RESULT 1480
 ID ABL32362 standard; DNA; 15674 BP.
 DE Human immune system associated gene SEQ ID NO: 335.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 15674;
 Best Local Similarity 43.9%; Pred. No. 4.1e+02;
 RESULT 1481
 ID ABL34476 standard; DNA; 15674 BP.
 DE Human metastasis associated gene SEQ ID NO: 29.
 PN WO200177376-A2.
 PD 18-OCT-2001.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 15674;
 Best Local Similarity 43.9%; Pred. No. 4.1e+02;
 RESULT 1482
 ID ABL70513 standard; DNA; 15674 BP.
 DE Chemically treated cell signalling DNA sequence#202.
 PN WO200202807-A2.
 PD 10-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 15674;
 Best Local Similarity 43.9%; Pred. No. 4.1e+02;
 RESULT 1483
 ID ADS99737 standard; DNA; 15674 BP.
 DE Bisulphite treated human gene associated with metastasis #15.

PN US2003148327-A1.
 PD 07-AUG-2003.
 PA (OLEK/) OLEK A.
 PA (PIEP/) PIEPENBROCK C.
 PA (BERL/) BERLIN K.
 Query Match 1.5%; Score 34.8; DB 7; Length 15674;
 Best Local Similarity 43.9%; Pred. No. 4.1e+02;
 RESULT 1484
 ID ABL32191 standard; DNA; 17137 BP.
 DE Human immune system associated gene SEQ ID NO: 164.
 PN WO200200928-A2.
 PD 03-JAN-2002.
 PA (EPIG-) EPIGENOMICS AG.
 Query Match 1.5%; Score 34.8; DB 6; Length 17137;
 Best Local Similarity 47.3%; Pred. No. 4.3e+02;
 RESULT 1485
 ID ACN43972 standard; DNA; 47601 BP.
 DE Mouse genomic sequence mCG12024.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 1.5%; Score 34.8; DB 11; Length 47601;
 Best Local Similarity 50.0%; Pred. No. 8.5e+02;
 RESULT 1486
 ID ABZ66811 standard; DNA; 48221 BP.
 DE Orthosomycin biosynthetic gene cluster SEQ ID NO 280.
 PN WO200279505-A2.
 PD 10-OCT-2002.
 PA (ECOP-) ECOPIA BIOSCIENCES INC.
 Query Match 1.5%; Score 34.8; DB 10; Length 48221;
 Best Local Similarity 50.6%; Pred. No. 8.6e+02;
 RESULT 1487
 Query Match 1.5%; Score 34.8; DB 10; Length 110000;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 RESULT 1488
 ID ADL13649 standard; DNA; 127098 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #181.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 1.5%; Score 34.8; DB 10; Length 127098;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 RESULT 1489
 ID ABD32851 standard; DNA; 181413 BP.
 DE Mouse cancer-associated genomic DNA MD17-032.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.5%; Score 34.8; DB 13; Length 181413;
 Best Local Similarity 48.9%; Pred. No. 2e+03;
 RESULT 1490
 ID ADQ97421 standard; DNA; 228835 BP.
 DE Human cancer associated sequence HD08-046, SEQ ID 398.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 1.5%; Score 34.8; DB 12; Length 228835;

Best Local Similarity 53.7%; Pred. No. 2.3e+03;
 RESULT 1491
 ID ABX49902 standard; cDNA; 317 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #15067.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 1.5%; Score 34.6; DB 8; Length 317;
 Best Local Similarity 50.6%; Pred. No. 35;
 RESULT 1492
 ID ABX49371 standard; cDNA; 320 BP.
 DE Bovine EST associated with lactation/muscle/fat deposition #14536.
 PN US2002137139-A1.
 PD 26-SEP-2002.
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 Query Match 1.5%; Score 34.6; DB 8; Length 320;
 Best Local Similarity 52.4%; Pred. No. 35;
 RESULT 1493
 ID ACN59310 standard; cDNA; 416 BP.
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-029-Q6-N6-B6, SEQ:14091.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 1.5%; Score 34.6; DB 13; Length 416;
 Best Local Similarity 53.7%; Pred. No. 42;
 RESULT 1494
 ID ADC93274 standard; DNA; 528 BP.
 DE E. faecium DNA sequence SEQ ID 2901.
 PN US6583275-B1.
 PD 24-JUN-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 1.5%; Score 34.6; DB 10; Length 528;
 Best Local Similarity 58.1%; Pred. No. 49;
 RESULT 1495
 ID ACN56850 standard; cDNA; 637 BP.
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-011-Q6-K6-E2, SEQ:11631.
 PN US2004123340-A1.
 PD 24-JUN-2004.
 PA (DEIK/) DEIKMAN J.
 PA (FENG/) FENG P C C.
 PA (FINC/) FINCHER K L.
 PA (ZIEG/) ZIEGLER T E.
 Query Match 1.5%; Score 34.6; DB 13; Length 637;
 Best Local Similarity 51.6%; Pred. No. 56;
 RESULT 1496
 ID ABZ32076 standard; DNA; 645 BP.
 DE Candida albicans essential gene SEQ ID NO 6363.
 PN WO200253728-A2.

PD 11-JUL-2002.

PA (ELIT-) ELITRA PHARM INC.

Query Match 1.5%; Score 34.6; DB 6; Length 645;

Best Local Similarity 44.8%; Pred. No. 56;

RESULT 1497

ID ADR60325 standard; cDNA; 646 BP.

DE Cotton cDNA sequence, SEQ ID 1106.

PN US2004181830-A1.

PD 16-SEP-2004.

PA (KOVA/) KOVALIC D K.

PA (ZHOU/) ZHOU Y.

PA (CAOY/) CAO Y.

Query Match 1.5%; Score 34.6; DB 13; Length 646;

Best Local Similarity 53.7%; Pred. No. 56;

RESULT 1498

ID AAS52930 standard; DNA; 771 BP.

DE Enterococcus faecalis DNA for cellular proliferation protein #358.

PN WO200170955-A2.

PD 27-SEP-2001.

PA (ELIT-) ELITRA PHARM INC.

Query Match 1.5%; Score 34.6; DB 4; Length 771;

Best Local Similarity 51.6%; Pred. No. 63;

RESULT 1499

ID ABT42401 standard; DNA; 1008 BP.

DE Toxicity modelling related rat gene SEQ ID No 2103.

PN WO200295000-A2.

PD 28-NOV-2002.

PA (GENE-) GENE LOGIC INC.

Query Match 1.5%; Score 34.6; DB 10; Length 1008;

Best Local Similarity 54.3%; Pred. No. 75;

RESULT 1500

ID ADP72800 standard; DNA; 1008 BP.

DE Renal toxin progression gene marker #1389.

PN WO2004048598-A2.

PD 10-JUN-2004.

PA (GENE-) GENE LOGIC INC.

Query Match 1.5%; Score 34.6; DB 12; Length 1008;

Best Local Similarity 54.3%; Pred. No. 75;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 06:28:57 ; Search time 407 Seconds
(without alignments)
9327.179 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 aggggtcccttagccgggcg.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8							
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
1	1147.8	49.5	2426	4	US-09-774-528-26	Sequence 26, Appl	
2	143.2	6.2	2966	4	US-09-976-594-241	Sequence 241, App	
3	137	5.9	1629	4	US-09-949-016-2596	Sequence 2596, Ap	
4	137	5.9	1708	4	US-09-949-016-2595	Sequence 2595, Ap	
5	136.4	5.9	2107	3	US-09-180-852-1	Sequence 1, Appli	
6	136	5.9	1832	4	US-09-949-016-2734	Sequence 2734, Ap	
7	136	5.9	1854	4	US-09-356-806-39	Sequence 39, Appl	
8	131.6	5.7	2092	4	US-09-356-806-7	Sequence 7, Appli	
9	130	5.6	2092	4	US-09-949-016-2594	Sequence 2594, Ap	
10	130	5.6	2092	4	US-09-949-016-3181	Sequence 3181, Ap	
11	128.4	5.5	1976	4	US-09-356-806-112	Sequence 112, App	

	12	127.6	5.5	1413	3	US-09-813-918-1	Sequence 1, Appli
	13	127.6	5.5	1413	4	US-10-060-311-1	Sequence 1, Appli
	14	125.2	5.4	2093	4	US-09-949-016-1128	Sequence 1128, Ap
	15	119.6	5.2	2351	4	US-09-949-016-76	Sequence 76, Appl
	16	119.6	5.2	2351	4	US-09-949-016-1813	Sequence 1813, Ap
	17	118	5.1	2336	5	PCT-US92-00282-1	Sequence 1, Appli
	18	115.4	5.0	1323	4	US-09-949-016-2735	Sequence 2735, Ap
	19	115.4	5.0	1323	4	US-09-949-016-2736	Sequence 2736, Ap
	20	111.2	4.8	2339	5	PCT-US92-00282-2	Sequence 2, Appli
	21	95.6	4.1	735	4	US-09-305-856B-17	Sequence 17, Appl
	22	79.2	3.4	7218	1	US-08-232-463-14	Sequence 14, Appl
	23	68.2	2.9	769	4	US-09-270-767-2063	Sequence 2063, Ap
	24	68.2	2.9	769	4	US-09-270-767-17345	Sequence 17345, A
c	25	64.6	2.8	1369	4	US-09-270-767-13787	Sequence 13787, A
	26	63.8	2.8	689	4	US-09-356-806-5	Sequence 5, Appli
	27	63.8	2.8	19732	4	US-09-949-016-12870	Sequence 12870, A
	28	63.8	2.8	19732	4	US-09-949-016-14923	Sequence 14923, A
	29	63.8	2.8	19733	4	US-09-949-016-14336	Sequence 14336, A
	30	62.4	2.7	391	3	US-09-370-838-21	Sequence 21, Appl
	31	62.4	2.7	391	4	US-09-854-133-21	Sequence 21, Appl
	32	62.2	2.7	1591	4	US-09-356-806-44	Sequence 44, Appl
	33	62.2	2.7	20441	4	US-09-949-016-14476	Sequence 14476, A
	34	59	2.5	18373	4	US-09-949-016-14338	Sequence 14338, A
	35	59	2.5	18452	4	US-09-949-016-14337	Sequence 14337, A
c	36	57.4	2.5	831	4	US-09-270-767-29825	Sequence 29825, A
	37	56.8	2.4	1731	2	US-08-466-583-1	Sequence 1, Appli
	38	56.8	2.4	1731	4	US-08-265-427-1	Sequence 1, Appli
	39	56.8	2.4	1731	5	PCT-US95-07820-1	Sequence 1, Appli
	40	56.2	2.4	513	4	US-09-270-767-14001	Sequence 14001, A
	41	56.2	2.4	983	4	US-09-671-317-386	Sequence 386, App
	42	55.8	2.4	350	4	US-09-513-999C-3284	Sequence 3284, Ap
	43	55	2.4	1602	4	US-09-356-806-117	Sequence 117, App
	44	55	2.4	20599	4	US-09-949-016-14477	Sequence 14477, A
	45	55	2.4	20599	4	US-09-949-016-14478	Sequence 14478, A
	46	53.4	2.3	783	5	PCT-US92-00282-22	Sequence 22, Appl
	47	53.4	2.3	17020	4	US-09-949-016-11818	Sequence 11818, A
	48	53.4	2.3	17021	4	US-09-949-016-13555	Sequence 13555, A
	49	49.2	2.1	657	4	US-09-669-751-104	Sequence 104, App
	50	48.8	2.1	1141	4	US-09-806-708B-22	Sequence 22, Appl
	51	48.6	2.1	1001	4	US-09-671-317-404	Sequence 404, App
c	52	46	2.0	41737	4	US-09-949-016-12204	Sequence 12204, A
c	53	46	2.0	41741	4	US-09-949-016-16983	Sequence 16983, A
	54	44.6	1.9	762	3	US-09-615-192A-218	Sequence 218, App
c	55	44.6	1.9	1141	4	US-09-806-708B-22	Sequence 22, Appl
	56	43.6	1.9	1001	4	US-09-671-317-413	Sequence 413, App
	57	43.6	1.9	1001	4	US-09-671-317-414	Sequence 414, App
	58	43.6	1.9	1001	4	US-09-671-317-415	Sequence 415, App
	59	43.6	1.9	1001	4	US-09-671-317-417	Sequence 417, App
	60	43.6	1.9	1021	4	US-09-356-806-115	Sequence 115, App
	61	43.2	1.9	1001	4	US-09-671-317-416	Sequence 416, App
	62	42.6	1.8	2025	3	US-08-942-012B-23	Sequence 23, Appl
	63	42	1.8	408	4	US-09-270-767-1461	Sequence 1461, Ap
	64	42	1.8	408	4	US-09-270-767-16743	Sequence 16743, A
	65	42	1.8	1800	6	5180581-1	Patent No. 5180581
	66	42	1.8	1800	6	5180581-1	Patent No. 5180581
	67	42	1.8	2793	1	US-08-281-916-5	Sequence 5, Appli
	68	42	1.8	2793	2	US-08-460-725-7	Sequence 7, Appli

Qy	458	ATGGATTCCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTTTGACTACTGT	517
Db	1	ATGGACTTCTTAAAAAATGAGAACTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGT	60
Qy	518	CCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTCCACTTCATTC	577
Db	61	TCTTTGCTAATTGTTGAAAAGCTTGGGAAACGATTTGTGTCCTTCTCCCTTCAATTT	120
Qy	578	GGCTCTTTGGAATTTGGGCTACCAA---TCCCCTTGTCTTATGTTCCAGTATTCCGTTCC	634
Db	121	AGCTATATGGACTTTGGGTTACCAAGCGCCCCCTTGTCTATGCTCCAGTGATGGTTCT	180
Qy	635	TTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTAGT	694
Db	181	GGTCTAACTGACCAAAATGGACTTCTGGGGCCGAGTGAAGAATTTCTGATGTTCTTGAT	240
Qy	695	TTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGAACATTTT	754
Db	241	TTCTCCATGAAGCAAAGGGGAAATCCTTTCTCAGTATGACAGCACTATCCAGGAGCATTTT	300
Qy	755	ACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATT	814
Db	301	GTGGAAGGCTCTCAGCCAGTGTGTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTGTC	360
Qy	815	AACTCTGACTTTGCTTTTGATTTTGTCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGA	874
Db	361	AACTCTGACTTTGCTTTTGATTTTGTCTCGTCCCTGTTTCCCAACACAGTCTATGTGGGA	420
Qy	875	GGCTTGATGGAAAAACCTATTAAACCAGTACCACAAGACTTGAGAACTTCATTGCCAAG	934
Db	421	GGTTTACTGGACAAACCTGTTTACGCCAATACCCAAGACTTGAGAAATTTTATCTCTCAG	480
Qy	935	TTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAAT	994
Db	481	TTTGGAGACTCAGGTTTTGTCTTGTGGCCCTGGGCTCTATAGTGAGCATGATTCAGTCC	540
Qy	995	CCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG	1054
Db	541	AAGGAAATTATTAAGGAGATGAACAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGG	600
Qy	1055	AAGTGTCACTGTTCTCATTGGCCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTG	1114
Db	601	ACATGTAAGACTTCTCATTGGCCCCAAAGATGTGAGTTTGGCCCCAAATGTCAAAATCATG	660
Qy	1115	GACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCACCCAC	1174
Db	661	GATTGGCTTCCACAGACTGACCTTCTAGCTCACCTAGCATTCGTCTGTTTGTCACTCAT	720
Qy	1175	GGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCT	1234
Db	721	GGAGGGATGAACAGTGTGATGGAGGCTGTCCATCATGGAGTACCCATGGTGGGGATTCCA	780
Qy	1235	CTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCT	1294
Db	781	TTTTTTTTTGACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTCT	840

Qy 1295 ATTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAA 1354
 ||||| || ||| ||||| ||||| ||||| || || || || ||||| ||||| |||
 Db 841 ATTCAGCTACAGACGCTCAAGGCAGAGTCATTTGCGCTCACCATGAAAAAATCATAGAA 900
 Qy 1355 GACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCCACCCGCTC 1414
 ||||| ||||| || ||| ||||| || || || || ||||| ||||| |||
 Db 901 GACAAGAGGTACAAGTCTGCAGCAATGGCCTCCAAGATTATCAGGCACTCCCACCCACTG 960
 Qy 1415 AGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACG 1474
 | ||| | ||| |||| | ||||| || || || || ||||| ||||| || |
 Db 961 ACCCCTGCCAGAGGCTTTTGGGCTGGATAGATCATATCTTGCAGACAGGGGGTGCAGCA 1020
 Qy 1475 CACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTT 1534
 || ||||| |||| || ||||| ||||| ||||| || || || || ||
 Db 1021 CATCTCAAGCCATATGCTTTCAGCAGCCATGGCATGAGCAGTACATGCTTGATGTCTTC 1080
 Qy 1535 GTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATG 1594
 | |||| || ||||| ||||| ||| | ||||| ||| ||| ||| |
 Db 1081 CTCTTCTCCTAGGGCTCATGCTGGGTACTTTGTGGCTTAGTGTAAGGTTCTTGTTGCT 1140
 Qy 1595 GCTGTCTGGTGGCTGCGTGGGGCCAGAAAGGTGAAGGAGACATAA 1639
 | | ||| ||| || || | |||| | |||| | ||||
 Db 1141 GTAACCAGGTATCTGAGTATAGCAACGAAGGTCAAGGAGGCATAA 1185

RESULT 8

AK041045

LOCUS AK041045 1353 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530069C13 product:hypothetical UDP-glucuronosyl and UDP-glucosyl transferase containing protein, full insert sequence.

ACCESSION AK041045

VERSION AK041045.1 GI:26334156

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1353)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .1353

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM_DB:A530069C13"

/db_xref="taxon:10090"

/clone="A530069C13"

```

/sex="male"
/tissue_type="aorta and vein"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
83. .991
/note="unnamed protein product; hypothetical
UDP-glucuronosyl and UDP-glucosyl transferase containing
protein (InterPro|IPR002213, evidence: InterPro)
putative"
/codon_start=1
/protein_id="BAC30796.1"
/db_xref="GI:26334157"
/translation="MAAHRRWLLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQ
VLHGEGHNVTKLLYESANIPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEEITYG
RSKHHTLLKIHQYFGDLCSQLLSRKDIMDFLKNENFDLVLLDSMDLCSLLIVEKLGR
.FVSLFPFQFSYMDFGLPSAPLSYAPVYGSLTDQMDFWGRVKNFLMFLDFSMKQREIL
SQYDSTIQEHFVEGSQPVLSDLLLKAELWVNSDFALDFARPLFPNTVYVGGYWTNLF
SQPKTWRILSLSLQVLSLWPWAL"

```

Query Match 31.5%; Score 731.6; DB 3; Length 1353;
Best Local Similarity 73.1%; Pred. No. 5.6e-196;
Matches 981; Conservative 0; Mismatches 354; Indels 7; Gaps 3;

Qy	1	AGGGTCCCTTAGCCGGGCGCAGGGCGCGAGCCAGGCTGAGATCCGCGGCTTCCGTAGA	60
Db	16	AGGGTCCCTTAGTGGGGCACAGCTCTTTAGGTGTGCAACCTGTGTCAGGGCTCCACATAT	75
Qy	61	AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCCT	120
Db	76	TCTACAGATGGCAGCACATCGGCGTTGGCTTCTCATGAGCTTCCTTTTCCCTTGAGGTTAT	135
Qy	121	GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT	180
Db	136	TCTCTTGGAGGCTGCAAAAATCCTGACTATATCTACACTGAGTGCAAGCCATTATATAGT	195
Qy	181	GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA	240
Db	196	GATAAGCCGTGTGTGCGCAAGTTCTTCATGAAGGTGGCCACAATGTGACCAAACTTCTTTA	255
Qy	241	CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAGGAAGAAAATCATATCAAGTTATCAG	300
Db	256	TGAAA---GTGCTAATATCCAGATTTTAGAAAGGAAAACCATCATATCAAGTTATTAA	312
Qy	301	TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAGAGTTTGGATTCTTTCTGGA	360
Db	313	TTGGCGTCCACCTGAAGATCAGGAAAAGAAATTTGCTGATCTTAGGCATCGACTTACAGA	372
Qy	361	AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC	420
Db	373	AGAAATAACTTATGGCAGGTCCAAACATCACACCCTTCTAAAGATCCATCAATACTTTGG	432
Qy	421	GTTGCAGTGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCTTAAAGAATGAGAA	480
Db	433	GGACTTATGCAGTCAATTATTAAGCAGAAAGGACATCATGGACTTCTTAAAAAATGAGAA	492
Qy	481	CTTCGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT	540

Db 493 CTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGTTCTTTGCTAATTGTTGAAAAGCT 552
 Qy 541 TGGGAAGCCATTGTGGCCATTCTTTCCACTTCATTCGGCTCTTTGGAATTTGGGCTACC 600
 Db 553 TGGGAAACGATTGTGTCCCTTCTTCCCTTTCAATTTAGCTATATGGACTTTGGGTTACC 612
 Qy 601 AA---TCCCCTTGCTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTT 657
 Db 613 AAGCGCCCCCTTGCTCTATGCTCCAGTGTATGGTTCTGGTCTAACTGACCAAATGGACTT 672
 Qy 658 CTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACAT 717
 Db 673 CTGGGGCCGAGTGAAGAACTTTCTGATGTTCCCTTGATTTCTCCATGAAGCAAAGGGAAAT 732
 Qy 718 GCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTTT 777
 Db 733 CCTTCTCAGTATGACAGCACTATCCAGGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTT 792
 Qy 778 GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGACTTTGCCTTTGATTT 837
 Db 793 GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGACTTTGCTTTGGATTT 852
 Qy 838 TGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAA 897
 Db 853 TGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGG-TTACTGGACAAACCTGTTCA 911
 Qy 898 ACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGACTCTGGTTTTGTCTT 957
 Db 912 GCCAATACCCCAAGACTTGGAGAATTTTATCTCTCAGTTTGGAGACTCAGGTTTTGTCTT 971
 Qy 958 TGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATCTTCAAGGAGATGAA 1017
 Db 972 TGTGGCCCTGGGCTCTATAGTGAGCATGATTCAAGTCCAAGGAAATTTATTAAGGAGATGAA 1031
 Qy 1018 CAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAGTGTCTCATTGGCC 1077
 Db 1032 CAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAGACTTCTCATTGGCC 1091
 Qy 1078 CAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTTCTCAGAGTGACCT 1137
 Db 1092 CAAAGATGTGAGTTTGGCCCCAAATGTCAAAATCATGGATTGGCTTCCACAGACTGACCT 1151
 Qy 1138 CCTGGCTCACCCCAAGCATCCGTCTGTTTGTCAACACGGCGGGCAGAATAGCATAATGGA 1197
 Db 1152 TCTAGCTCACCTAGCATTCGTCTGTTTGTCACTCATGGAGGGATGAACAGTGTGATGGA 1211
 Qy 1198 GGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGAGACCAGCCTGAAAA 1257
 Db 1212 GGCTGTCCATCATGGAGTACCCATGGTGGGGATTCCATTTTTTTTTTGACCAACCTGAAAA 1271
 Qy 1258 CATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTGAGTTAAAGAAGCTCAAGGC 1317
 Db 1272 CATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTATTGAGTACAGACGCTCAAGGC 1331
 Qy 1318 AGAGACATTGGCTCTTAAGATG 1339

Qy 764 TCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTCTGAC 823
 ||| ||||| ||||| | ||||| ||||| | ||||| |||||
 Db 121 TCTCAGCCAGTGTTGTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGAC 180

Qy 824 TTTGCCTTTGATTTTGTCTGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATG 883
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 TTTGCCTTTGATTTTGTCTCGTCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTG 240

Qy 884 GAAAAACCTATTAAACAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTTTGGGGAC 943
 || ||||| || | ||| ||||| ||||| ||||| | ||| || | ||||| |||||
 Db 241 GACAAACCTGTTCAAGCAATACCCCAAGACTTGGAGGATTTTATCTCTCAGTTTGGAGAC 300

Qy 944 TCTGGTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGAATCCGGAAATC 1003
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 301 TCAGGTTTGTCTTGTGGCCCTGGACTCTGTAGTGAGCATGATTCAAGTCCAAGGAAAT 360

Qy 1004 TTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGGAAGTGTGAG 1063
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 361 ATTAAGGAGATGAACAGTGCCTTTGCTCACCTCCCTCAAGGGGTGCTATGGACATGTAAG 420

Qy 1064 TGTTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTGGACTGGCTT 1123
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 421 AGTTCTCATTGGCCCAAAGATGTGAGTTTGGCCCAAATGTCAAAATCATGGATTGGCTT 480

Qy 1124 CCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTCAACCCACGGCGGGCAG 1183
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 481 CCACAGATTGACCTTCTAGCTCACCTTAGCATTCGTCTGTTTGTCAACCATGGGGGGATG 540

Qy 1184 AATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTTGGA 1243
 || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 541 AACAGTGTAAATGGAGGCTGTCCATCATGGAGTACCAATGGTAGGGATTCCATTTTGGGA 600

Qy 1244 GACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTAGTTA 1303
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 601 GACCAACCTGAAAACATGGTCCGAGTAGAAGCAAAGAACCTTGGTGTCTTATTAGCTA 660

Qy 1304 AAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGA 1363
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 661 CAGACACTCAAGGCAGAGTCATTTTGGCTCACCATGAAAGAAGTCATAGAAGACCAGAGG 720

Qy 1364 TACAAGTCCGCGGCAGTGGCTGCCAGTGTGATCCTGCGCTCCCAACCGCTCAGCCCCACA 1423
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 721 TACAAGACTGCAGCA-TGGCCTCCAAGGTTATCAGGAACTCCCAACC--AATGACCCTGGC 777

Qy 1424 CAGCGGCTGGTGGGCTGGATTGACCACGTC-CTCCAGACAGGGGGCGCGACGCACCTCAA 1482
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 778 CAGAGGCTTGTGGGCTGGATTGATCACATCTTGCAGACAGGGGGTGCAGCCCATCTCAA 837

Qy 1483 GCCCTATGTCTT-TCAGCAGCCCTGGCATGAGCAGTAC 1519
 | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 838 AGCATATGGCTTCCCAAGCAGGCTTGGCATAACGAGTAC 875

RESULT 10

CN396939

LOCUS CN396939

510 bp

mRNA

linear

EST 16-MAY-2004

DEFINITION 17000599940872 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN396939
 VERSION CN396939.1 GI:47384534
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 510)
 AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J and Stanton, L.W.
 TITLE Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 510 Std Error: 0.00.
 FEATURES
 source Location/Qualifiers
 1. .510
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and
 mitogen-treated hES cell line H7"
 /clone_lib="GRN_PRENEU"
 /note="oligo dT primed, full-length enriched cDNA library
 from hES cell line H7 (p29) maintained in feeder-free
 conditions. Embryoid bodies were generated in the presence
 of all-trans retinoic and mitogens."

ORIGIN

Query Match 21.8%; Score 506.4; DB 7; Length 510;
 Best Local Similarity 99.8%; Pred. No. 4.5e-132;
 Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1109 ATGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTC 1168
 |||
 Db 3 ATGTGGACTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTGTC 62
 Qy 1169 ACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGG 1228
 |||
 Db 63 ACCCACGGCGGGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGG 122
 Qy 1229 ATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGT 1288
 |||
 Db 123 ATCCCTCTCTTTGGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGT 182
 Qy 1289 GTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 1348
 |||
 Db 183 GTTCTATTTCAGTTAAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATC 242
 Qy 1349 ATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCAC 1408


```

|||||
Db      243 ATGGAAGACAAGAGATACAAGTCCGCGGCAGTGGCTGCCAGTGTTCATCCTGCGCTCCCAC 302
Qy      1409 CCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGC 1468
|||||
Db      303 CCGCTCAGCCCCACACAGCGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGC 362
Qy      1469 GCGACGCGACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGAC 1528
|||||
Db      363 GCGACGCGACCTCAAGCCCTATGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGCTCGAC 422
Qy      1529 GTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTG 1588
|||||
Db      423 GTTTTGTGTTTCTGCTGGGGCTCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTG 482
Qy      1589 GGCATGGCTGTCTGGTGGCTGCGTGGGG 1616
|||||
Db      483 GGCATGGCTGTCTGGTGGCTGCGTGGGG 510

```

RESULT 11

CR769328

LOCUS CR769328 717 bp mRNA linear EST 23-SEP-2004

DEFINITION DKFZp46900528_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKFZp46900528 5', mRNA sequence.

ACCESSION CR769328

VERSION CR769328.1 GI:52613343

KEYWORDS EST.

SOURCE Pongo pygmaeus (orangutan)

ORGANISM Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

REFERENCE 1 (bases 1 to 717)

AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaipp,A.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.

TITLE Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,
Deutschenbaur,S., et al.)

JOURNAL Unpublished (2004)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
(Martinsried/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp46900528) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:

<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp46900528>

Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

source

Location/Qualifiers

1. .717

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

Db 664 GGAGCCCNATGGGGACATGCAGTCTACATTTGGACAACNCCNTCAAGGAGCATT 717

RESULT 12
BI559553'

LOCUS BI559553 761 bp mRNA linear EST 05-SEP-2001
DEFINITION 603252894F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295502 5',
mRNA sequence.

ACCESSION BI559553
VERSION BI559553.1 GI:15446867
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 761)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11747 row: k column: 23
High quality sequence stop: 726.

FEATURES Location/Qualifiers
source 1. .761
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5295502"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 21.1%; Score 488.6; DB 4; Length 761;
Best Local Similarity 80.7%; Pred. No. 6.1e-127;
Matches 608; Conservative 0; Mismatches 139; Indels 6; Gaps 3;

Qy 8 CTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAGTGAGC 67

Source	Position	Sequence	Position
Db	6	CTTAGCCCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCTGCTTCTGTGGAAGTGAGC	65
Qy	68	ATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTGCTCTCA	127
Db	66	ATGGTTGGGCAGCGGGTGCTGCTTCTAGTGGCCTTCCTTCTTTCTGGGGTCTGCTCTCA	125
Qy	128	GAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGAC	187
Db	126	GAGGCTGCCAAAATCCTGACAATATCTACACTGGGTGGAAGCCATTACCTACTGTTGGAC	185
Qy	188	CGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGA	247
Db	186	CGGGTGTCTCAGATTCTTCAAGAGCATGGTCATAATGTGACTATGCTTCATCAGAGTGGA	245
Qy	248	GGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTT	307
Db	246	AAGTTTTGGATCCCAGATATTAAAGAGGAGGAAAAATCATACCAAGTTATCAGGTGGTTT	305
Qy	308	GCACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACT	367
Db	306	TCACCTGAAGATCATCAAAAAAGAATTAAGAAGCATTTTGATAGCTACATAGAAACAGCA	365
Qy	368	TTAGGTGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAG	427
Db	366	TTGGATGGCAGAAAAGAATCTGAAGCCCTTGTAAGCTAATGGAAATATTTGGGACTCAA	425
Qy	428	TGCAGTCATTTTTTAAATAGAAAGGATATCATGGATTCCCTTAAAGAATGAGAACTTCGAC	487
Db	426	TGTAGTTATTTGCTAAGCAGAAAGGATATAATGGATTCCCTTAAAGAATGAGAACTATGAT	485
Qy	488	ATGGTGATAGTTGAA-ACTTTTGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAA	546
Db	486	CTGGTATTTGTTGAACGCATTTGATTTCTGTTCTTTCTGATTGCTGAGAAGCTTGTGAA	545
Qy	547	GCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCC	606
Db	546	ACCATTTGTGGCCATTCTTCCCACCACATTTCGGCTCTATGGATTTGGGGCTACCAAGCCC	605
Qy	607	CTTGTCTTATGTTCCAGTATTCCGTTCCCTTGCTGACT-GATCACATGGACTTCTGGGGCC	665
Db	606	CTTGTCTTATGTTCCAGTATTCCCTTCCCTTGCTGACTGGATCACATGGACTTCTGGGGCC	665
Qy	666	GAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGG----CAACAGCACATGCAG	721
Db	666	GAGTGAAGAAATTTCTGATGTCTTTAGTTTCTCCTCAAGGAGCCCAATGGGACATGCAG	725
Qy	722	TCTACATTTGACAACACCATCAAGGAACATTTT	754
Db	726	TCTACAATTTGACAACACATCAAGGAGCATTTT	758

2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE PRECURSOR ; ,
mRNA sequence.

ACCESSION AW173071

VERSION AW173071.1 GI:6439019

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 694)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 412.

FEATURES Location/Qualifiers

source 1. .694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2663780"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 20.0%; Score 463.6; DB 2; Length 694;
Best Local Similarity 83.5%; Pred. No. 7.7e-120;
Matches 537; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

Qy	268	TAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCACCTGAAGATCATCAAAG	327
Db	643	TATAAGAGAAGCAAAATTCATACAGGTATCCGGTGGTTTTCACCTAAGATCATCAAAA	584
Qy	328	AGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGGTGGCAGAGGAAAAATT	387
Db	583	AGAA-TTAAGAAGCATTTTGATAGCTACATAGAAACAGCATTTGGATGGCAGAAAAGAATC	525
Qy	388	TGAAAACTTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTCATTTTTTAAATAG	447
Db	524	TGAAGCCCTTGTAAGCTAATGGAAATATTTGGGACTCAATGTAGTTATTTGCTAAGCAG	465

Qy	448	AAAGGATATCATGGATTCCCTTAAAGAATGAGAACTTCGACATGGTGATAGTTGAAACTTT	507
Db	464	AAAGGATATAATGGATTCCCTTAAAGAATGAGAACTATGATCTGGTATTTGTTGAAGCATT	405
Qy	508	TGACTACTGTCCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGCCATTCTTTC	567
Db	404	TGATTTCTGTTCTTTCTGATTGCTGAGAAGCTTGTGAAACCATTTGTGGCCATTCTTCC	345
Qy	568	CACTTCATTTCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCCAGTATT	627
Db	344	CACCACATTCGGCTCTTTGGATTTTGGGCTACCAAGCCCCTTGTCTTATGTTCCAGTATT	285
Qy	628	CCGTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTT	687
Db	284	CCCTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTGATGTT	225
Qy	688	CTTTAGTTTCTGCAGGAGGCCAACAGCACATGCAGTCTACATTTGACAACACCATCAAGGA	747
Db	224	CTTTAGTTTCTCCAGGAGCCAATGGGACATGCAGTCTACATTTGACAACACCATCAAGGA	165
Qy	748	ACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTG	807
Db	164	GCATTTCCAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGTG	105
Qy	808	GTTCAATTAACCTCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTA	867
Db	104	GTTTGTTAACTCTGATTTTGCTTTGATTTTGCCCGGCCCTGCTTCCCAACACTGTTTA	45
Qy	868	TGTTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAA	910
Db	44	TATTGGAGGCTTGATGGAAAAACCTATTAAACCAGTACCACAA	2

Db 178 ATCACCAAATTTGGAGACTCTGGTTTTGTCCTTGTAAGCCTGGGGTCCATGGTGAGTTTC 119

Qy 986 TGTCAGAATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGG 1045
 || | | || | |||| ||||| ||||| || || |||||

Db 118 ATTCGGTCCCAGGAGTTCTCAAAGAGATGAATGCTGCCTTTGCTCATCTCCCTCAAGGG 59

Qy 1046 GTGATATGGAAGTGTCTAGTGTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAA 1101
 ||||| ||||| | | ||||| ||||| || | |||| ||||

Db 58 GTGATATGGAAGTATAATCCTTCTCATTGGCCCAAAGACATCAAATTGGCCCCAAA 3

RESULT 15

AK052644

LOCUS AK052644 1723 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630011D02 product:hypothetical UDP-glucoronosyl and UDP-glucosyl transferase containing protein, full insert sequence.

ACCESSION AK052644

VERSION AK052644.1 GI:26095303

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1723)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.

FEATURES

source Location/Qualifiers

1. .1723

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM_DB:D630011D02"

/db_xref="taxon:10090"

/clone="D630011D02"

/tissue_type="kidney"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="0 day neonate"

misc_feature

1. .1723

/note="hypothetical UDP-glucoronosyl and UDP-glucosyl transferase containing protein (InterPro|IPR002213, evidence: InterPro)"

ORIGIN

Query Match 19.5%; Score 452.6; DB 3; Length 1723;

Best Local Similarity 69.1%; Pred. No. 1.5e-116;

Matches 649; Conservative 0; Mismatches 284; Indels 6; Gaps 2;

Qy 1 AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGA 60

|||||

Db 41 AGGGTCCCTTAGTGGGGCACAGCTCTTTAGGTGTGCAACCTGTGTGAGGGCTCCACATAT 100

Qy 61 AGTGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCT 120
| | | | | | | | | | | | | | | | | | | | | |

Db 101 TCTACAGATGGCAGCACATCGGCGTTGGCTTCTCATGAGCTTCCTTTTCTTGAGGTTAT 160

Qy 121 GCTCTCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACT 180
| | | | | | | | | | | | | | | | | | | | | |

Db 161 TCTCTTGAGGCTGCAAAAATCCTGACTATATCTACACTGAGTGCAAGCCATTATATAGT 220

Qy 181 GATGGACCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCA 240
| | | | | | | | | | | | | | | | | | | | | |

Db 221 GATAAGCCGTGTGTCGCAAGTCTTTCATGAAGGTGGCCACAATGTGACCAAACTTCTTTA 280

Qy 241 CAAAAGAGGTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAG 300
| | | | | | | | | | | | | | | | | | | | | |

Db 281 TGAAA---GTGCTAATATCCAGATTTTAGAAAGGAAAAACCATCATATCAAGTTATTAA 337

Qy 301 TTGGCTTGACCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTCTTTCTGGA 360
| | | | | | | | | | | | | | | | | | | | | |

Db 338 TTGGCGTCCACCTGAAGATCAGGAAAAGAAATTTGCTGATCTTAGGCATCGACTTACAGA 397

Qy 361 AGAAACTTTAGGTGGCAGAGGAAAATTTGAAACTTATTAAATGTTCTAGAATACTTGGC 420
| | | | | | | | | | | | | | | | | | | | | |

Db 398 AGAAATAACTTATGGCAGGTCCAAACATCACACCCTTCTAAAGATCCATCAATACTTTGG 457

Qy 421 GTTGCAGTGCAGTCATTTTTTAAATAGAAAAGGATATCATGGATTCCCTTAAAGAATGAGAA 480
| | | | | | | | | | | | | | | | | | | | | |

Db 458 GGACTTATGCAGTCAATTATTAAGCAGAAAAGGACATCATGGACTTCTTAAAAAATGAGAA 517

Qy 481 CTTGACATGGTGATAGTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCT 540
| | | | | | | | | | | | | | | | | | | | | |

Db 518 CTTTGACCTAGTACTTCTTGATTCAATGGATCTCTGTTCTTTGCTAATTGTTGAAAAGCT 577

Qy 541 TGGGAAGCCATTTGTGGCCATTCTTTCCACTTCATTTCGGCTCTTTGGAATTTGGGGTACC 600
| | | | | | | | | | | | | | | | | | | | | |

Db 578 TGGGAAACGATTTGTGTCTTTCTTCCCTTTCAATTTAGCTATATGGACTTTGGGGTACC 637

Qy 601 AA---TCCCCTTGTCTTATGTTCCAGTATTCGGTTCCTTGCTGACTGATCACATGGACTT 657
| | | | | | | | | | | | | | | | | | | | | |

Db 638 AAGCGCCCCCTTGTCTATGCTCCAGTGTATGGTTCTGGTCTAACTGACCAAATGGACTT 697

Qy 658 CTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACAT 717
| | | | | | | | | | | | | | | | | | | | | |

Db 698 CTGGGGCCGAGTGAAGAATTTTCTGATGTTCTTTGATTCTCCATGAAGCAAAGGGAAAT 757

Qy 718 GCAGTCTACATTTGACAACACCATCAAGGAACATTTACAGAAGGCTCTAGGCCAGTTTT 777
| | | | | | | | | | | | | | | | | | | | | |

Db 758 CCTTCTCAGTATGACAGCACTATCCAGGAGCATTTTGTGGAAGGCTCTCAGCCAGTGTT 817

Qy 778 GTCTCATCTTCTACTGAAAGCAGAGTTGTGGTTCATTAACCTGACTTTGCCCTTTGATTT 837
| | | | | | | | | | | | | | | | | | | | | |

Db 818 GTCTGACCTTCTACTGAAAGCTGAGCTGTGGTTTGTCAACTCTGACTTTGCTTTGGATTT 877

Qy 838 TGCTCGACCTCTGCTTCCCAACACTGTTTATGTTGGAGGCTTGATGGAAAAACCTATTAA 897
| | | | | | | | | | | | | | | | | | | | | |

Db 878 TGCTCGTCCCCTGTTTCCCAACACAGTCTATGTGGGAGGTTTACTGGACAAACCTGTTCA 937

Qy 898 ACCAGTACCACAAGACTTGGAGAACTTCATTGCCAAGTT 936
 | | | | | | | | | | | | | | | | | | | | |
Db 938 GCCAATACCCCAAGTAAGTGACAAATTAGCTCTCACTTT 976

Search completed: February 15, 2005, 09:44:23
Job time : 6858 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2005, 06:24:06 ; Search time 4625 Seconds
(without alignments)
2959.798 Million cell updates/sec

Title: US-10-017-867A-281
Perfect score: 2320
Sequence: 1 aggggtcccttagccggggcgc.....tctctccccaacctcactaa 2320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
37	2320	100.0	2320	16	US-10-013-909A-281	Sequence 281, App
66	2102.8	90.6	2944	17	US-10-468-125-13	Sequence 13, Appl
67	2063.4	88.9	2074	9	US-09-822-830A-262	Sequence 262, App
68	1578.8	68.1	2263	17	US-10-381-898-31	Sequence 31, Appl
69	1281.6	55.2	2082	9	US-09-895-728-1	Sequence 1, Appli
70	1281.6	55.2	2823	17	US-10-094-749-1288	Sequence 1288, Ap
71	1280	55.2	2086	17	US-10-258-080-12	Sequence 12, Appl
72	1270.4	54.8	1851	9	US-09-740-029-1	Sequence 1, Appli
73	1212	52.2	1572	9	US-09-895-728-3	Sequence 3, Appli
74	1147.8	49.5	2426	17	US-10-120-988-26	Sequence 26, Appl
c 75	708.2	30.5	1898	17	US-10-276-774-1313	Sequence 1313, Ap
76	593.4	25.6	1842	17	US-10-104-047-811	Sequence 811, App
c 77	441	19.0	923	17	US-10-295-027-677	Sequence 677, App
78	433.6	18.7	42999	9	US-09-740-029-3	Sequence 3, Appli
79	319.4	13.8	981	10	US-09-764-891-1668	Sequence 1668, Ap
80	239.2	10.3	5973	10	US-09-764-891-8352	Sequence 8352, Ap
c 81	238.8	10.3	507	9	US-09-864-761-13591	Sequence 13591, A
82	238.8	10.3	2751	10	US-09-764-891-8351	Sequence 8351, Ap
83	238.8	10.3	5974	10	US-09-764-891-8353	Sequence 8353, Ap
c 84	220	9.5	277	9	US-09-864-761-30130	Sequence 30130, A
85	164.2	7.1	708	13	US-10-027-632-98682	Sequence 98682, A
86	164.2	7.1	708	17	US-10-027-632-98682	Sequence 98682, A
87	162.6	7.0	49753	13	US-10-087-192-1855	Sequence 1855, Ap
88	159.6	6.9	625	13	US-10-027-632-95784	Sequence 95784, A
89	159.6	6.9	625	13	US-10-027-632-95785	Sequence 95785, A
90	159.6	6.9	625	13	US-10-027-632-95786	Sequence 95786, A
91	159.6	6.9	625	17	US-10-027-632-95784	Sequence 95784, A
92	159.6	6.9	625	17	US-10-027-632-95785	Sequence 95785, A
93	159.6	6.9	625	17	US-10-027-632-95786	Sequence 95786, A
94	145.2	6.3	1961	9	US-09-917-800A-1403	Sequence 1403, Ap
95	144.2	6.2	1584	9	US-09-962-678-3	Sequence 3, Appli
96	144.2	6.2	1584	17	US-10-184-648-40	Sequence 40, Appl
97	144.2	6.2	3006	9	US-09-962-678-1	Sequence 1, Appli
98	144.2	6.2	3006	17	US-10-184-648-38	Sequence 38, Appl
99	143.2	6.2	1636	9	US-09-981-353-165	Sequence 165, App
100	143.2	6.2	1636	17	US-10-258-080-11	Sequence 11, Appl
101	143.2	6.2	2966	9	US-09-981-353-33	Sequence 33, Appl
564	143.2	6.2	2974	16	US-10-174-587-521	Sequence 521, App
621	143.2	6.2	2974	18	US-10-643-795A-3	Sequence 3, Appli
622	141.8	6.1	336	11	US-09-864-408A-941	Sequence 941, App
623	141.8	6.1	1947	17	US-10-152-319A-2121	Sequence 2121, Ap
624	141.6	6.1	1705	17	US-10-114-270-51	Sequence 51, Appl
625	141.2	6.1	1620	14	US-10-158-646-45	Sequence 45, Appl
626	141	6.1	3050	17	US-10-114-270-49	Sequence 49, Appl
627	140	6.0	1593	17	US-10-152-319A-1908	Sequence 1908, Ap
628	140	6.0	2634	17	US-10-388-934-169	Sequence 169, App
629	139.8	6.0	1639	17	US-10-468-125-18	Sequence 18, Appl
630	139.2	6.0	1714	9	US-09-981-353-193	Sequence 193, App
631	139.2	6.0	1855	9	US-09-880-107-2120	Sequence 2120, Ap
632	139.2	6.0	1855	11	US-09-968-007A-368	Sequence 368, App
633	139.2	6.0	1855	11	US-09-968-007A-735	Sequence 735, App
634	139.2	6.0	1855	18	US-10-783-528-57	Sequence 57, Appl
635	139.2	6.0	1991	14	US-10-057-834A-1	Sequence 1, Appli

636	136.4	5.9	1844	14	US-10-175-523-59	Sequence 59, Appl
637	136.4	5.9	2448	9	US-09-967-768A-187	Sequence 187, App
638	136	5.9	1854	14	US-10-205-522-39	Sequence 39, Appl
639	133.8	5.8	1894	17	US-10-172-118-904	Sequence 904, App
640	133.8	5.8	1894	17	US-10-342-887-904	Sequence 904, App
641	133.4	5.8	1756	15	US-10-235-994-27	Sequence 27, Appl
642	133.2	5.7	1829	16	US-10-252-157-24	Sequence 24, Appl
643	133	5.7	1662	17	US-10-307-817-117	Sequence 117, App
644	132	5.7	1614	17	US-10-381-898-24	Sequence 24, Appl
645	131.6	5.7	2092	14	US-10-205-522-7	Sequence 7, Appli
646	130	5.6	2123	9	US-09-880-107-3286	Sequence 3286, Ap
647	129	5.6	2799	9	US-09-880-107-3756	Sequence 3756, Ap
648	128.4	5.5	1976	14	US-10-205-522-112	Sequence 112, App
649	128.4	5.5	2090	9	US-09-880-107-3292	Sequence 3292, Ap
650	127.6	5.5	1413	13	US-10-060-311-1	Sequence 1, Appli
651	127.6	5.5	1413	18	US-10-778-300-1	Sequence 1, Appli
652	127.2	5.5	2150	9	US-09-981-353-45	Sequence 45, Appl
653	127.2	5.5	2150	16	US-10-252-157-25	Sequence 25, Appl
654	125.2	5.4	2093	9	US-09-880-107-3842	Sequence 3842, Ap
655	124.2	5.4	2844	14	US-10-198-846-13134	Sequence 13134, A
656	124	5.3	1889	9	US-09-981-353-83	Sequence 83, Appl
657	121.2	5.2	1712	9	US-09-981-353-189	Sequence 189, App
658	121.2	5.2	1712	14	US-10-158-646-42	Sequence 42, Appl
659	120.6	5.2	1224	17	US-10-381-898-32	Sequence 32, Appl
660	119.6	5.2	2349	9	US-09-981-353-151	Sequence 151, App
661	119.6	5.2	2349	13	US-10-044-090-845	Sequence 845, App
662	115.8	5.0	2422	9	US-09-880-107-2106	Sequence 2106, Ap
663	115.8	5.0	2422	11	US-09-968-007A-750	Sequence 750, App
664	112.8	4.9	2368	17	US-10-240-425-1321	Sequence 1321, Ap
665	112.8	4.9	2380	13	US-10-044-090-816	Sequence 816, App
666	112.8	4.9	2385	9	US-09-981-353-153	Sequence 153, App
667	111.4	4.8	2320	9	US-09-835-082-1	Sequence 1, Appli
668	111.4	4.8	2320	9	US-09-835-082-3	Sequence 3, Appli
669	111.4	4.8	2320	17	US-10-333-108-6	Sequence 6, Appli
670	111.4	4.8	2320	18	US-10-422-522-35	Sequence 35, Appl
671	111	4.8	1593	18	US-10-250-508-18	Sequence 18, Appl
672	111	4.8	1593	18	US-10-250-508-19	Sequence 19, Appl
673	111	4.8	1593	18	US-10-250-508-20	Sequence 20, Appl
674	111	4.8	1593	18	US-10-250-508-21	Sequence 21, Appl
675	110	4.7	811	14	US-10-198-846-10821	Sequence 10821, A
676	97	4.2	1593	17	US-10-152-319A-2064	Sequence 2064, Ap
677	95.6	4.1	735	9	US-09-305-856B-17	Sequence 17, Appl
678	95.6	4.1	735	16	US-10-247-159-17	Sequence 17, Appl
679	93.2	4.0	54493	13	US-10-087-192-1858	Sequence 1858, Ap
680	86.2	3.7	419	9	US-09-960-352-9640	Sequence 9640, Ap
681	86.2	3.7	874	17	US-10-332-859-134	Sequence 134, App
682	86.2	3.7	1318	17	US-10-332-859-296	Sequence 296, App
683	76.8	3.3	426	9	US-09-960-352-13860	Sequence 13860, A
684	75.8	3.3	418	9	US-09-960-352-10064	Sequence 10064, A
685	74.6	3.2	603	9	US-09-917-800A-1434	Sequence 1434, Ap
686	74	3.2	582	9	US-09-867-701-1453	Sequence 1453, Ap
c 687	73.8	3.2	918	13	US-10-027-632-146775	Sequence 146775,
c 688	73.8	3.2	918	17	US-10-027-632-146775	Sequence 146775,
689	72	3.1	450	14	US-10-198-846-1381	Sequence 1381, Ap
690	70.8	3.1	601	9	US-09-917-800A-1433	Sequence 1433, Ap
691	69.2	3.0	350	9	US-09-960-352-2069	Sequence 2069, Ap
692	69.2	3.0	381	9	US-09-960-352-2070	Sequence 2070, Ap

693	66.8	2.9	416	9	US-09-960-352-12236	Sequence 12236, A
694	63.8	2.8	500	9	US-09-864-761-8163	Sequence 8163, Ap
695	63.8	2.8	689	14	US-10-205-522-5	Sequence 5, Appli
696	63.6	2.7	370	9	US-09-960-352-3236	Sequence 3236, Ap
697	63.4	2.7	378	9	US-09-960-352-1300	Sequence 1300, Ap
698	63.4	2.7	396	14	US-10-066-543-2912	Sequence 2912, Ap
699	63.4	2.7	569	13	US-10-027-632-187724	Sequence 187724,
700	63.4	2.7	569	17	US-10-027-632-187724	Sequence 187724,
701	62.4	2.7	391	9	US-09-738-973-21	Sequence 21, Appl
702	62.4	2.7	391	9	US-09-854-133-21	Sequence 21, Appl
703	62.4	2.7	391	15	US-10-144-649A-21	Sequence 21, Appl
704	62.4	2.7	417	9	US-09-960-352-11024	Sequence 11024, A
705	62.2	2.7	1591	14	US-10-205-522-44	Sequence 44, Appl
706	60.8	2.6	1751	18	US-10-437-963-38200	Sequence 38200, A
707	60.2	2.6	196	9	US-09-960-352-3013	Sequence 3013, Ap
708	60	2.6	220	9	US-09-864-761-24905	Sequence 24905, A
709	59.4	2.6	1606	17	US-10-042-865-27	Sequence 27, Appl
710	59.4	2.6	1606	17	US-10-072-012-151	Sequence 151, App
c 711	59	2.5	589	9	US-09-864-761-14859	Sequence 14859, A
c 712	58.6	2.5	753	18	US-10-425-115-95645	Sequence 95645, A
713	58.6	2.5	1555	18	US-10-437-963-83376	Sequence 83376, A
c 714	58.6	2.5	2071	18	US-10-739-930-2568	Sequence 2568, Ap
715	58.2	2.5	432	14	US-10-066-543-3166	Sequence 3166, Ap
716	57.4	2.5	1515	18	US-10-437-963-97778	Sequence 97778, A
717	57.2	2.5	646	18	US-10-767-701-1823	Sequence 1823, Ap
718	56.8	2.4	987	17	US-10-425-114-31066	Sequence 31066, A
719	56.8	2.4	1391	17	US-10-425-114-20377	Sequence 20377, A
720	56.8	2.4	1679	18	US-10-425-115-6301	Sequence 6301, Ap
721	56.8	2.4	1761	18	US-10-739-930-2527	Sequence 2527, Ap
722	56.2	2.4	983	17	US-10-294-934-386	Sequence 386, App
723	55.4	2.4	1637	18	US-10-425-115-174192	Sequence 174192,
c 724	55.2	2.4	203	9	US-09-864-761-31386	Sequence 31386, A
725	55.2	2.4	2541	18	US-10-425-115-174195	Sequence 174195,
726	55	2.4	1602	14	US-10-205-522-117	Sequence 117, App
727	54.2	2.3	1380	16	US-10-167-547C-21	Sequence 21, Appl
728	53.8	2.3	531	15	US-10-259-165-700	Sequence 700, App
729	53.8	2.3	849	18	US-10-425-115-32911	Sequence 32911, A
730	53.8	2.3	1380	16	US-10-167-547C-23	Sequence 23, Appl
731	53.8	2.3	1904	17	US-10-424-599-106506	Sequence 106506,
732	53.4	2.3	577	16	US-10-029-386-13232	Sequence 13232, A
733	53.4	2.3	629	18	US-10-767-701-24016	Sequence 24016; A
734	53.4	2.3	784	17	US-10-333-108-8	Sequence 8, Appli
735	53.4	2.3	1701	17	US-10-425-114-28222	Sequence 28222, A
736	53.4	2.3	1705	18	US-10-425-115-137865	Sequence 137865,
737	53.4	2.3	17483	18	US-10-751-606-1	Sequence 1, Appli
738	53.2	2.3	393	9	US-09-960-352-8259	Sequence 8259, Ap
739	53.2	2.3	549	18	US-10-437-963-18130	Sequence 18130, A
740	53.2	2.3	1883	17	US-10-424-599-139633	Sequence 139633,
741	52.8	2.3	383	9	US-09-960-352-1313	Sequence 1313, Ap
c 742	52.4	2.3	643	18	US-10-425-115-115184	Sequence 115184,
743	52	2.2	707	18	US-10-357-930-24702	Sequence 24702, A
744	52	2.2	1162	18	US-10-425-115-14963	Sequence 14963, A
745	51.8	2.2	963	17	US-10-425-114-19881	Sequence 19881, A
746	51.8	2.2	1688	17	US-10-425-114-23090	Sequence 23090, A
747	51.8	2.2	1952	18	US-10-425-115-38737	Sequence 38737, A
748	51.6	2.2	405	18	US-10-425-115-11581	Sequence 11581, A
749	51.6	2.2	781	18	US-10-425-115-154997	Sequence 154997,

750	51.6	2.2	994	17	US-10-424-599-141645	Sequence 141645,
751	51.6	2.2	1664	17	US-10-425-114-25165	Sequence 25165, A
752	51.6	2.2	1781	17	US-10-425-114-27714	Sequence 27714, A
753	51.6	2.2	1851	18	US-10-425-115-73099	Sequence 73099, A
754	51.2	2.2	1536	17	US-10-425-114-13903	Sequence 13903, A
755	51.2	2.2	1585	18	US-10-425-115-83913	Sequence 83913, A
756	51	2.2	1428	18	US-10-437-963-48509	Sequence 48509, A
757	51	2.2	1741	17	US-10-425-114-17536	Sequence 17536, A
c 758	51	2.2	1924	18	US-10-437-963-36431	Sequence 36431, A
759	51	2.2	2041	18	US-10-425-115-41669	Sequence 41669, A
c 760	50.8	2.2	1090	18	US-10-767-701-9917	Sequence 9917, Ap
c 761	50.8	2.2	1708	18	US-10-425-115-6686	Sequence 6686, Ap
762	50.6	2.2	1409	18	US-10-437-963-26987	Sequence 26987, A
763	50.4	2.2	493	18	US-10-767-701-29807	Sequence 29807, A
764	50.4	2.2	647	18	US-10-767-701-7103	Sequence 7103, Ap
765	50.4	2.2	1064	18	US-10-767-701-6787	Sequence 6787, Ap
766	50.4	2.2	1536	17	US-10-359-369-21	Sequence 21, Appl
767	50.4	2.2	1575	17	US-10-359-369-26	Sequence 26, Appl
c 768	50.4	2.2	1582	18	US-10-437-963-54318	Sequence 54318, A
769	50.4	2.2	1601	13	US-10-078-929-71	Sequence 71, Appl
770	50.2	2.2	627	15	US-10-259-165-135	Sequence 135, App
771	50.2	2.2	659	18	US-10-425-115-49556	Sequence 49556, A
772	50.2	2.2	1389	17	US-10-424-599-64785	Sequence 64785, A
773	50.2	2.2	1511	18	US-10-437-963-99212	Sequence 99212, A
c 774	50.2	2.2	1649	18	US-10-739-930-2332	Sequence 2332, Ap
775	50	2.2	947	18	US-10-739-930-3855	Sequence 3855, Ap
776	50	2.2	1052	17	US-10-425-114-24020	Sequence 24020, A
777	50	2.2	1358	18	US-10-425-115-146230	Sequence 146230,
778	49.8	2.1	743	18	US-10-425-115-125571	Sequence 125571,
779	49.8	2.1	1711	18	US-10-739-930-2421	Sequence 2421, Ap
780	49.6	2.1	398	13	US-10-078-929-67	Sequence 67, Appl
781	49.6	2.1	563	18	US-10-357-930-37283	Sequence 37283, A
782	49.6	2.1	932	13	US-10-078-929-65	Sequence 65, Appl
783	49.6	2.1	1603	17	US-10-425-114-34547	Sequence 34547, A
784	49.6	2.1	1627	17	US-10-425-114-20731	Sequence 20731, A
785	49.6	2.1	1840	18	US-10-425-115-126489	Sequence 126489,
c 786	49.2	2.1	600	18	US-10-425-115-81788	Sequence 81788, A
787	49.2	2.1	656	9	US-09-768-020-77	Sequence 77, Appl
788	49.2	2.1	657	14	US-10-255-536-104	Sequence 104, App
789	49.2	2.1	891	17	US-10-425-114-30590	Sequence 30590, A
790	49.2	2.1	1619	17	US-10-425-114-21697	Sequence 21697, A
791	49.2	2.1	1784	18	US-10-425-115-136164	Sequence 136164,
792	49.2	2.1	1807	17	US-10-425-114-28103	Sequence 28103, A
793	49.2	2.1	1943	18	US-10-425-115-122168	Sequence 122168,
794	49	2.1	501	18	US-10-357-930-7320	Sequence 7320, Ap
795	49	2.1	1052	15	US-10-259-165-668	Sequence 668, App
c 796	49	2.1	1058	18	US-10-767-701-6477	Sequence 6477, Ap
797	49	2.1	1491	18	US-10-437-963-52288	Sequence 52288, A
c 798	48.8	2.1	558	11	US-09-969-034-4441	Sequence 4441, Ap
799	48.8	2.1	1448	17	US-10-425-114-23975	Sequence 23975, A
800	48.8	2.1	1721	18	US-10-425-115-55704	Sequence 55704, A
c 801	48.6	2.1	875	18	US-10-437-963-54314	Sequence 54314, A
802	48.6	2.1	1001	17	US-10-294-934-404	Sequence 404, App
803	48.6	2.1	1647	18	US-10-739-930-2506	Sequence 2506, Ap
804	48.6	2.1	2142	18	US-10-437-963-26615	Sequence 26615, A
805	48.4	2.1	1437	9	US-09-938-842A-200	Sequence 200, App
806	48.4	2.1	1437	11	US-09-938-842A-200	Sequence 200, App

807	48.4	2.1	1638	17	US-10-425-114-1736	Sequence 1736, Ap
808	48.4	2.1	1785	18	US-10-739-930-2178	Sequence 2178, Ap
c 809	48.4	2.1	1796	18	US-10-437-963-15077	Sequence 15077, A
810	48.4	2.1	1828	18	US-10-425-115-146232	Sequence 146232,
c 811	48.2	2.1	551	15	US-10-259-165-483	Sequence 483, App
c 812	48.2	2.1	551	17	US-10-260-238-4854	Sequence 4854, Ap
813	48.2	2.1	916	17	US-10-425-114-14455	Sequence 14455, A
814	48.2	2.1	1827	17	US-10-425-114-21585	Sequence 21585, A
815	48.2	2.1	2112	18	US-10-425-115-57104	Sequence 57104, A
816	48	2.1	666	18	US-10-767-701-3341	Sequence 3341, Ap
817	48	2.1	1494	18	US-10-437-963-61715	Sequence 61715, A
818	48	2.1	1560	18	US-10-437-963-55774	Sequence 55774, A
819	48	2.1	1630	17	US-10-425-114-35120	Sequence 35120, A
820	47.8	2.1	719	18	US-10-767-701-19394	Sequence 19394, A
821	47.8	2.1	1138	9	US-09-974-300-897	Sequence 897, App
822	47.8	2.1	1461	18	US-10-437-963-80973	Sequence 80973, A
c 823	47.8	2.1	1474	18	US-10-437-963-67002	Sequence 67002, A
824	47.8	2.1	1844	18	US-10-425-115-11583	Sequence 11583, A
c 825	47.8	2.1	1934	18	US-10-437-963-102103	Sequence 102103,
c 826	47.6	2.1	706	17	US-10-424-599-139514	Sequence 139514,
827	47.6	2.1	1485	17	US-10-425-114-23053	Sequence 23053, A
828	47.6	2.1	1540	18	US-10-425-115-136162	Sequence 136162,
829	47.6	2.1	1805	18	US-10-739-930-4281	Sequence 4281, Ap
830	47.4	2.0	1784	18	US-10-437-963-88455	Sequence 88455, A
831	47.2	2.0	1215	17	US-10-425-114-33967	Sequence 33967, A
832	47.2	2.0	1215	18	US-10-425-115-107730	Sequence 107730,
833	47.2	2.0	1882	17	US-10-425-114-15891	Sequence 15891, A
834	47.2	2.0	1902	18	US-10-425-115-130862	Sequence 130862,
c 835	47	2.0	523	18	US-10-425-115-84886	Sequence 84886, A
836	47	2.0	1455	18	US-10-437-963-8361	Sequence 8361, Ap
837	47	2.0	1746	17	US-10-425-114-32779	Sequence 32779, A
838	46.8	2.0	429	18	US-10-767-701-2000	Sequence 2000, Ap
839	46.8	2.0	629	18	US-10-767-701-7057	Sequence 7057, Ap
840	46.6	2.0	334	9	US-09-981-353-149	Sequence 149, App
841	46.6	2.0	334	14	US-10-158-646-43	Sequence 43, Appl
c 842	46.6	2.0	634	15	US-10-259-165-476	Sequence 476, App
843	46.6	2.0	1416	18	US-10-425-115-90291	Sequence 90291, A
844	46.6	2.0	2050	18	US-10-767-701-13466	Sequence 13466, A
845	46.4	2.0	315	9	US-09-960-352-5852	Sequence 5852, Ap
846	46.4	2.0	1440	9	US-09-938-842A-80	Sequence 80, Appl
847	46.4	2.0	1440	11	US-09-938-842A-80	Sequence 80, Appl
848	46.4	2.0	1440	17	US-10-359-369-11	Sequence 11, Appl
849	46.4	2.0	1440	17	US-10-203-319A-10	Sequence 10, Appl
c 850	46.4	2.0	1440	17	US-10-203-319A-12	Sequence 12, Appl
851	46.4	2.0	1865	18	US-10-739-930-1152	Sequence 1152, Ap
852	46.2	2.0	1410	18	US-10-437-963-97054	Sequence 97054, A
853	46.2	2.0	1430	17	US-10-425-114-27279	Sequence 27279, A
854	46.2	2.0	1464	18	US-10-425-115-100628	Sequence 100628,
855	46.2	2.0	1694	18	US-10-437-963-42666	Sequence 42666, A
856	46.2	2.0	1762	17	US-10-425-114-27635	Sequence 27635, A
857	46.2	2.0	1999	18	US-10-437-963-85175	Sequence 85175, A
858	46	2.0	1557	18	US-10-437-963-18533	Sequence 18533, A
859	46	2.0	1973	18	US-10-437-963-97633	Sequence 97633, A
860	45.8	2.0	592	18	US-10-425-115-117281	Sequence 117281,
861	45.8	2.0	1188	18	US-10-437-963-101308	Sequence 101308,
862	45.8	2.0	1353	18	US-10-437-963-47687	Sequence 47687, A
863	45.8	2.0	1395	18	US-10-437-963-101310	Sequence 101310,

864	45.8	2.0	1473	18	US-10-437-963-47689	Sequence 47689, A
865	45.8	2.0	13511	15	US-10-311-455-254	Sequence 254, App
866	45.8	2.0	18585	15	US-10-240-485-162	Sequence 162, App
867	45.6	2.0	1770	17	US-10-425-114-15851	Sequence 15851, A
868	45.6	2.0	1780	18	US-10-425-115-181935	Sequence 181935, A
869	45.6	2.0	2319	18	US-10-437-963-50152	Sequence 50152, A
870	45.4	2.0	614	18	US-10-767-701-875	Sequence 875, App
871	45.4	2.0	661	18	US-10-767-701-4653	Sequence 4653, Ap
872	45.4	2.0	1674	17	US-10-425-114-15925	Sequence 15925, A
873	45.4	2.0	1699	18	US-10-437-963-52771	Sequence 52771, A
874	45.4	2.0	1722	18	US-10-425-115-168238	Sequence 168238, A
875	45.2	1.9	242	9	US-09-923-876-847	Sequence 847, App
876	45.2	1.9	242	10	US-09-923-876-847	Sequence 847, App
c 877	45.2	1.9	507	18	US-10-425-115-180382	Sequence 180382, A
878	45.2	1.9	1624	17	US-10-425-114-15834	Sequence 15834, A
879	45.2	1.9	1634	18	US-10-425-115-180642	Sequence 180642, A
880	45.2	1.9	1728	18	US-10-425-115-56280	Sequence 56280, A
881	45.2	1.9	1736	13	US-10-078-929-79	Sequence 79, Appl
882	45.2	1.9	1796	18	US-10-437-963-7426	Sequence 7426, Ap
883	45.2	1.9	5335	18	US-10-437-963-18859	Sequence 18859, A
920	45	1.9	45	16	US-10-013-909A-285	Sequence 285, App
949	45	1.9	503	18	US-10-425-115-89379	Sequence 89379, A
950	45	1.9	1515	17	US-10-359-369-30	Sequence 30, Appl
951	45	1.9	1536	9	US-09-773-882-10	Sequence 10, Appl
952	45	1.9	1560	17	US-10-359-369-33	Sequence 33, Appl
953	45	1.9	1732	9	US-09-773-882-1	Sequence 1, Appli
954	44.8	1.9	1362	9	US-09-938-842A-2417	Sequence 2417, Ap
955	44.8	1.9	1362	11	US-09-938-842A-2417	Sequence 2417, Ap
956	44.8	1.9	1473	18	US-10-437-963-70764	Sequence 70764, A
957	44.8	1.9	1867	18	US-10-437-963-41728	Sequence 41728, A
958	44.8	1.9	2323	18	US-10-437-963-88877	Sequence 88877, A
c 959	44.6	1.9	661	18	US-10-425-115-119313	Sequence 119313, A
960	44.6	1.9	762	15	US-10-174-693-218	Sequence 218, App
961	44.6	1.9	1437	17	US-10-359-369-17	Sequence 17, Appl
c 962	44.6	1.9	1803	18	US-10-425-115-109154	Sequence 109154, A
963	44.6	1.9	2532	18	US-10-437-963-80263	Sequence 80263, A
c 964	44.4	1.9	1607	18	US-10-425-115-58267	Sequence 58267, A
965	44.4	1.9	2166	17	US-10-425-114-18441	Sequence 18441, A
966	44.2	1.9	314	18	US-10-425-115-115658	Sequence 115658, A
c 967	44.2	1.9	576	18	US-10-425-115-122874	Sequence 122874, A
968	44.2	1.9	1449	18	US-10-437-963-33526	Sequence 33526, A
969	44.2	1.9	3750	18	US-10-437-963-53143	Sequence 53143, A
970	44	1.9	481	17	US-10-425-114-3555	Sequence 3555, Ap
971	44	1.9	1593	18	US-10-437-963-40777	Sequence 40777, A
972	44	1.9	1696	17	US-10-425-114-28610	Sequence 28610, A
973	44	1.9	1811	18	US-10-425-115-95638	Sequence 95638, A
974	43.8	1.9	1152	15	US-10-259-165-201	Sequence 201, App
975	43.8	1.9	1494	18	US-10-437-963-95025	Sequence 95025, A
976	43.8	1.9	1594	17	US-10-424-599-8655	Sequence 8655, Ap
977	43.8	1.9	1660	17	US-10-425-114-24406	Sequence 24406, A
978	43.8	1.9	1665	17	US-10-425-114-26967	Sequence 26967, A
979	43.8	1.9	1806	18	US-10-425-115-136538	Sequence 136538, A
980	43.8	1.9	1862	18	US-10-425-115-53664	Sequence 53664, A
981	43.8	1.9	2255	17	US-10-424-599-36266	Sequence 36266, A
982	43.8	1.9	513509	10	US-09-754-853A-4	Sequence 4, Appli
983	43.6	1.9	734	18	US-10-767-701-2409	Sequence 2409, Ap
984	43.6	1.9	1001	17	US-10-294-934-413	Sequence 413, App

985	43.6	1.9	1001	17	US-10-294-934-414	Sequence 414, App
986	43.6	1.9	1001	17	US-10-294-934-415	Sequence 415, App
987	43.6	1.9	1001	17	US-10-294-934-417	Sequence 417, App
988	43.6	1.9	1021	14	US-10-205-522-115	Sequence 115, App
989	43.6	1.9	1350	9	US-09-938-842A-1802	Sequence 1802, Ap
990	43.6	1.9	1350	11	US-09-938-842A-1802	Sequence 1802, Ap
991	43.6	1.9	1437	17	US-10-203-319A-47	Sequence 47, Appl
c 992	43.4	1.9	678	17	US-10-260-238-5409	Sequence 5409, Ap
993	43.4	1.9	679	18	US-10-767-701-10218	Sequence 10218, A
994	43.4	1.9	1518	18	US-10-437-963-21883	Sequence 21883, A
c 995	43.4	1.9	1929	18	US-10-437-963-10789	Sequence 10789, A
c 996	43.4	1.9	2300	18	US-10-437-963-3213	Sequence 3213, Ap
997	43.2	1.9	608	18	US-10-437-963-19715	Sequence 19715, A
998	43.2	1.9	753	18	US-10-437-963-53241	Sequence 53241, A
999	43.2	1.9	843	18	US-10-425-115-125569	Sequence 125569,
1000	43.2	1.9	1001	17	US-10-294-934-416	Sequence 416, App
1001	43.2	1.9	1425	18	US-10-437-963-81894	Sequence 81894, A
1002	43.2	1.9	1607	17	US-10-425-114-28586	Sequence 28586, A
1003	43.2	1.9	1636	18	US-10-425-115-76603	Sequence 76603, A
1004	43.2	1.9	10329	15	US-10-311-455-2095	Sequence 2095, Ap
1005	43.2	1.9	3673778	16	US-10-312-841-2	Sequence 2, Appli
1006	43	1.9	393	17	US-10-260-238-5737	Sequence 5737, Ap
c1007	43	1.9	1657	18	US-10-739-930-1829	Sequence 1829, Ap
1008	43	1.9	1683	17	US-10-424-599-72856	Sequence 72856, A
1009	42.8	1.8	494	18	US-10-767-701-29543	Sequence 29543, A
1010	42.8	1.8	588	18	US-10-767-701-21628	Sequence 21628, A
1011	42.8	1.8	849	18	US-10-425-115-177919	Sequence 177919,
1012	42.8	1.8	893	18	US-10-425-115-71067	Sequence 71067, A
1013	42.8	1.8	2295	17	US-10-424-599-50983	Sequence 50983, A
1016	42.6	1.8	1368	18	US-10-489-254-3	Sequence 3, Appli
c1017	42.6	1.8	1647	18	US-10-739-930-3269	Sequence 3269, Ap
1018	42.4	1.8	121	10	US-09-818-875-4016	Sequence 4016, Ap
c1019	42.4	1.8	121	10	US-09-818-875-4017	Sequence 4017, Ap
1020	42.4	1.8	121	17	US-10-209-787-4016	Sequence 4016, Ap
c1021	42.4	1.8	121	17	US-10-209-787-4017	Sequence 4017, Ap
1022	42.4	1.8	121	17	US-10-261-185-4016	Sequence 4016, Ap
c1023	42.4	1.8	121	17	US-10-261-185-4017	Sequence 4017, Ap
1024	42.4	1.8	121	18	US-10-681-074-4016	Sequence 4016, Ap
c1025	42.4	1.8	121	18	US-10-681-074-4017	Sequence 4017, Ap
1026	42.4	1.8	234	9	US-09-960-352-12264	Sequence 12264, A
1027	42.4	1.8	428	18	US-10-437-963-65973	Sequence 65973, A
c1028	42.4	1.8	747	17	US-10-424-599-137248	Sequence 137248,
1029	42.4	1.8	798	17	US-10-425-114-11594	Sequence 11594, A
1030	42.4	1.8	1410	17	US-10-203-319A-1	Sequence 1, Appli
c1031	42.4	1.8	1410	17	US-10-203-319A-3	Sequence 3, Appli
1032	42.4	1.8	1410	18	US-10-489-254-2	Sequence 2, Appli
1033	42.4	1.8	1413	18	US-10-437-963-73192	Sequence 73192, A
1034	42.4	1.8	1428	9	US-09-938-842A-2381	Sequence 2381, Ap
1035	42.4	1.8	1428	11	US-09-938-842A-2381	Sequence 2381, Ap
1036	42.4	1.8	1428	17	US-10-359-369-15	Sequence 15, Appl
1037	42.4	1.8	1430	17	US-10-203-319A-13	Sequence 13, Appl
c1038	42.4	1.8	1430	17	US-10-203-319A-15	Sequence 15, Appl
1039	42.4	1.8	1437	17	US-10-424-599-40441	Sequence 40441, A
1040	42.4	1.8	1620	18	US-10-437-963-11058	Sequence 11058, A
c1041	42.4	1.8	1747	18	US-10-437-963-87975	Sequence 87975, A
1042	42.4	1.8	2192	17	US-10-424-599-104632	Sequence 104632,
1043	42.4	1.8	2910	17	US-10-424-599-40437	Sequence 40437, A

1044	42.4	1.8	180557	13	US-10-003-806-6	Sequence 6, Appli
1045	42.4	1.8	180557	13	US-10-003-806-9	Sequence 9, Appli
1046	42.2	1.8	640	18	US-10-437-963-29554	Sequence 29554, A
1047	42.2	1.8	40862	15	US-10-311-455-2046	Sequence 2046, Ap
1048	42	1.8	1302	18	US-10-437-963-43996	Sequence 43996, A
1049	42	1.8	1365	18	US-10-437-963-31306	Sequence 31306, A
c1050	42	1.8	40324	18	US-10-433-793-180	Sequence 180, App
1051	41.8	1.8	795	17	US-10-424-599-128688	Sequence 128688,
1052	41.8	1.8	821	18	US-10-767-701-12684	Sequence 12684, A
1053	41.8	1.8	1494	18	US-10-437-963-6035	Sequence 6035, Ap
1054	41.8	1.8	1547	17	US-10-425-114-15608	Sequence 15608, A
1055	41.8	1.8	1591	18	US-10-425-115-8000	Sequence 8000, Ap
1056	41.8	1.8	1810	18	US-10-425-115-118492	Sequence 118492,
1057	41.6	1.8	849	18	US-10-425-115-158279	Sequence 158279,
1058	41.6	1.8	7238	15	US-10-311-455-421	Sequence 421, App
c1059	41.4	1.8	664	17	US-10-424-599-95100	Sequence 95100, A
1060	41.4	1.8	1003	17	US-10-424-599-23367	Sequence 23367, A
1061	41.4	1.8	1416	18	US-10-437-963-73968	Sequence 73968, A
1062	41.4	1.8	1434	17	US-10-203-319A-51	Sequence 51, Appl
c1063	41.4	1.8	1450	18	US-10-437-963-73966	Sequence 73966, A
1064	41.4	1.8	1637	17	US-10-425-114-4288	Sequence 4288, Ap
1065	41.4	1.8	1654	17	US-10-425-114-34899	Sequence 34899, A
1066	41.4	1.8	1730	17	US-10-425-114-26349	Sequence 26349, A
1067	41.4	1.8	1737	17	US-10-425-114-26388	Sequence 26388, A
1068	41.4	1.8	5130	18	US-10-425-115-28545	Sequence 28545, A
1069	41.2	1.8	711	18	US-10-425-115-173181	Sequence 173181,
1070	41.2	1.8	748	17	US-10-424-599-43682	Sequence 43682, A
c1071	41.2	1.8	765	17	US-10-424-599-54353	Sequence 54353, A
1072	41.2	1.8	1374	9	US-09-938-842A-1576	Sequence 1576, Ap
1073	41.2	1.8	1374	11	US-09-938-842A-1576	Sequence 1576, Ap
1074	41.2	1.8	1500	18	US-10-437-963-31808	Sequence 31808, A
c1075	41.2	1.8	1630	18	US-10-437-963-689	Sequence 689, App
1076	41.2	1.8	1648	17	US-10-424-599-131197	Sequence 131197,
1077	41.2	1.8	1693	17	US-10-424-599-139294	Sequence 139294,
1078	41.2	1.8	7829	15	US-10-311-455-1078	Sequence 1078, Ap
1079	41.2	1.8	7829	17	US-10-221-613-150	Sequence 150, App
1080	41.2	1.8	10710	15	US-10-311-455-866	Sequence 866, App
c1081	41	1.8	476	18	US-10-425-115-29545	Sequence 29545, A
1082	41	1.8	485	17	US-10-260-238-974	Sequence 974, App
c1083	41	1.8	538	17	US-10-424-599-128448	Sequence 128448,
c1084	41	1.8	99232	18	US-10-331-053-16	Sequence 16, Appl
c1085	41	1.8	99588	13	US-10-087-192-1780	Sequence 1780, Ap
1086	40.8	1.8	623	18	US-10-021-323-11890	Sequence 11890, A
1087	40.8	1.8	964	18	US-10-425-115-152977	Sequence 152977,
1088	40.8	1.8	1419	18	US-10-437-963-75846	Sequence 75846, A
1089	40.8	1.8	1485	18	US-10-437-963-44040	Sequence 44040, A
1090	40.8	1.8	1530	18	US-10-425-115-29163	Sequence 29163, A
1091	40.8	1.8	1788	18	US-10-739-930-4334	Sequence 4334, Ap
1092	40.8	1.8	2145	18	US-10-437-963-52766	Sequence 52766, A
c1093	40.8	1.8	1691139	14	US-10-067-514-1	Sequence 1, Appli
c1094	40.8	1.8	1691139	17	US-10-419-723-1	Sequence 1, Appli
1095	40.6	1.8	1684	18	US-10-425-115-58723	Sequence 58723, A
1096	40.6	1.8	3673778	16	US-10-312-841-1	Sequence 1, Appli
c1097	40.4	1.7	427	9	US-09-960-352-8924	Sequence 8924, Ap
c1098	40.4	1.7	951	18	US-10-425-115-3198	Sequence 3198, Ap
1099	40.4	1.7	1437	18	US-10-437-963-96474	Sequence 96474, A
1100	40.4	1.7	1440	18	US-10-489-254-6	Sequence 6, Appli

1101	40.4	1.7	1825	18	US-10-739-930-2896	Sequence 2896, Ap
1102	40.2	1.7	468	15	US-10-259-165-570	Sequence 570, App
1103	40.2	1.7	1428	18	US-10-437-963-6034	Sequence 6034, Ap
1104	40.2	1.7	1461	18	US-10-437-963-13634	Sequence 13634, A
1105	40.2	1.7	1497	18	US-10-437-963-31876	Sequence 31876, A
c1106	40.2	1.7	1817	18	US-10-437-963-6037	Sequence 6037, Ap
1107	40	1.7	526	18	US-10-425-115-35024	Sequence 35024, A
c1108	40	1.7	745	18	US-10-437-963-20740	Sequence 20740, A
1109	40	1.7	1401	18	US-10-437-963-56917	Sequence 56917, A
1110	40	1.7	1437	18	US-10-437-963-5180	Sequence 5180, Ap
1111	40	1.7	1457	17	US-10-203-319A-50	Sequence 50, Appl
1112	40	1.7	1524	17	US-10-425-114-16534	Sequence 16534, A
1113	40	1.7	1621	17	US-10-425-114-25554	Sequence 25554, A
1114	40	1.7	1684	18	US-10-425-115-27273	Sequence 27273, A
1115	40	1.7	1717	18	US-10-437-963-76344	Sequence 76344, A
1116	40	1.7	1926	18	US-10-425-115-71559	Sequence 71559, A
1117	40	1.7	1983	18	US-10-739-930-1013	Sequence 1013, Ap
1118	40	1.7	6029	15	US-10-311-455-1966	Sequence 1966, Ap
1119	40	1.7	7631	15	US-10-311-455-833	Sequence 833, App
1120	40	1.7	8576	15	US-10-311-455-2201	Sequence 2201, Ap
1121	40	1.7	10716	15	US-10-311-455-1391	Sequence 1391, Ap
1122	40	1.7	17389	15	US-10-311-455-1387	Sequence 1387, Ap
1123	39.8	1.7	664	13	US-10-027-632-198986	Sequence 198986,
1124	39.8	1.7	664	17	US-10-027-632-198986	Sequence 198986,
1125	39.8	1.7	697	18	US-10-767-701-8937	Sequence 8937, Ap
1126	39.8	1.7	902	18	US-10-767-701-14552	Sequence 14552, A
1127	39.8	1.7	1371	9	US-09-938-842A-1517	Sequence 1517, Ap
1128	39.8	1.7	1371	11	US-09-938-842A-1517	Sequence 1517, Ap
1129	39.8	1.7	1371	18	US-10-489-254-4	Sequence 4, Appli
1130	39.8	1.7	1407	17	US-10-260-238-1077	Sequence 1077, Ap
1131	39.8	1.7	1407	18	US-10-437-963-85974	Sequence 85974, A
1132	39.8	1.7	1437	17	US-10-203-319A-16	Sequence 16, Appl
c1133	39.8	1.7	1437	17	US-10-203-319A-18	Sequence 18, Appl
1134	39.8	1.7	1451	17	US-10-203-319A-48	Sequence 48, Appl
1135	39.8	1.7	1494	17	US-10-203-319A-54	Sequence 54, Appl
1136	39.8	1.7	1580	17	US-10-424-599-29544	Sequence 29544, A
1137	39.8	1.7	1892	17	US-10-424-599-14514	Sequence 14514, A
1138	39.8	1.7	2559	18	US-10-489-254-1	Sequence 1, Appli
c1139	39.6	1.7	563	17	US-10-424-599-43466	Sequence 43466, A
c1140	39.6	1.7	781	17	US-10-424-599-43469	Sequence 43469, A
c1141	39.6	1.7	899	17	US-10-424-599-139634	Sequence 139634,
1142	39.6	1.7	974	18	US-10-767-701-9283	Sequence 9283, Ap
1143	39.6	1.7	1250	17	US-10-425-114-31550	Sequence 31550, A
1144	39.6	1.7	1433	17	US-10-203-319A-49	Sequence 49, Appl
c1145	39.6	1.7	1434	18	US-10-437-963-59057	Sequence 59057, A
1146	39.6	1.7	1763	17	US-10-425-114-31892	Sequence 31892, A
1147	39.6	1.7	1775	17	US-10-424-599-27212	Sequence 27212, A
1148	39.6	1.7	2383	18	US-10-425-115-150283	Sequence 150283,
c1149	39.6	1.7	5858	19	US-10-488-056-14	Sequence 14, Appl
1150	39.6	1.7	6104	15	US-10-311-455-1340	Sequence 1340, Ap
c1151	39.6	1.7	31168	9	US-09-764-868-1464	Sequence 1464, Ap
1152	39.6	1.7	50937	10	US-09-808-880-1	Sequence 1, Appli
c1153	39.6	1.7	567564	18	US-10-699-156-3	Sequence 3, Appli
1154	39.4	1.7	637	18	US-10-767-701-23672	Sequence 23672, A
1155	39.4	1.7	1437	17	US-10-203-319A-34	Sequence 34, Appl
1156	39.4	1.7	1461	18	US-10-437-963-42491	Sequence 42491, A
1157	39.4	1.7	1524	18	US-10-425-115-111360	Sequence 111360,

1158	39.4	1.7	1540	18	US-10-425-115-143587	Sequence 143587,
1159	39.4	1.7	1837	18	US-10-425-115-64766	Sequence 64766, A
1160	39.4	1.7	2112	18	US-10-437-963-69524	Sequence 69524, A
1161	39.4	1.7	11155	15	US-10-311-455-578	Sequence 578, App
c1162	39.2	1.7	482	15	US-10-002-623-654	Sequence 654, App
1163	39.2	1.7	578	18	US-10-653-047-1248	Sequence 1248, Ap
1164	39.2	1.7	654	17	US-10-425-114-4843	Sequence 4843, Ap
1165	39.2	1.7	661	15	US-10-259-165-660	Sequence 660, App
1166	39.2	1.7	1148	18	US-10-425-115-42020	Sequence 42020, A
1167	39.2	1.7	1323	18	US-10-437-963-63672	Sequence 63672, A
1168	39.2	1.7	1350	18	US-10-437-963-46245	Sequence 46245, A
1169	39.2	1.7	1474	18	US-10-437-963-74077	Sequence 74077, A
1170	39.2	1.7	1512	18	US-10-437-963-60833	Sequence 60833, A
1171	39.2	1.7	1544	18	US-10-437-963-7661	Sequence 7661, Ap
1172	39.2	1.7	1803	18	US-10-437-963-5740	Sequence 5740, Ap
1173	39.2	1.7	2445	13	US-10-027-632-265388	Sequence 265388,
1174	39.2	1.7	2445	13	US-10-027-632-265389	Sequence 265389,
1175	39.2	1.7	2445	13	US-10-027-632-265390	Sequence 265390,
1176	39.2	1.7	2445	17	US-10-027-632-265388	Sequence 265388,
1177	39.2	1.7	2445	17	US-10-027-632-265389	Sequence 265389,
1178	39.2	1.7	2445	17	US-10-027-632-265390	Sequence 265390,
1179	39	1.7	503	17	US-10-260-238-4498	Sequence 4498, Ap
1180	39	1.7	759	9	US-09-305-856B-15	Sequence 15, Appl
1181	39	1.7	759	16	US-10-247-159-15	Sequence 15, Appl
1182	39	1.7	774	18	US-10-437-963-71913	Sequence 71913, A
1183	39	1.7	930	9	US-09-305-856B-13	Sequence 13, Appl
1184	39	1.7	930	16	US-10-247-159-13	Sequence 13, Appl
1185	39	1.7	1244	17	US-10-333-108-5	Sequence 5, Appli
1186	39	1.7	1452	17	US-10-333-108-4	Sequence 4, Appli
1187	39	1.7	1515	18	US-10-437-963-71467	Sequence 71467, A
1188	39	1.7	5807	15	US-10-311-455-1127	Sequence 1127, Ap
1189	39	1.7	7771	15	US-10-311-455-1945	Sequence 1945, Ap
1190	39	1.7	12753	17	US-10-041-018-19	Sequence 19, Appl
1194	38.8	1.7	475	18	US-10-767-701-30227	Sequence 30227, A
c1195	38.8	1.7	478	9	US-09-864-761-11467	Sequence 11467, A
c1196	38.8	1.7	482	15	US-10-002-623-651	Sequence 651, App
c1197	38.8	1.7	519	14	US-10-123-155-210	Sequence 210, App
1210	38.8	1.7	736	17	US-10-424-599-79064	Sequence 79064, A
1211	38.8	1.7	890	17	US-10-425-114-12405	Sequence 12405, A
c1212	38.8	1.7	890	18	US-10-425-115-91545	Sequence 91545, A
1213	38.8	1.7	1134	15	US-10-259-165-740	Sequence 740, App
1214	38.8	1.7	1134	17	US-10-260-238-5631	Sequence 5631, Ap
1215	38.8	1.7	1341	17	US-10-425-114-31564	Sequence 31564, A
1216	38.8	1.7	1373	17	US-10-425-114-1212	Sequence 1212, Ap
1217	38.8	1.7	1425	18	US-10-437-963-82290	Sequence 82290, A
1218	38.8	1.7	1437	18	US-10-425-115-42001	Sequence 42001, A
1219	38.8	1.7	1823	18	US-10-425-115-25921	Sequence 25921, A
1220	38.8	1.7	1990	18	US-10-425-115-132923	Sequence 132923,
1221	38.8	1.7	5820	15	US-10-311-455-512	Sequence 512, App
1222	38.8	1.7	7455	15	US-10-311-455-1731	Sequence 1731, Ap
1223	38.8	1.7	11049	15	US-10-311-455-642	Sequence 642, App
1224	38.8	1.7	11049	17	US-10-240-589C-28	Sequence 28, Appl
1225	38.8	1.7	11662	15	US-10-311-455-1873	Sequence 1873, Ap
c1226	38.8	1.7	3673778	16	US-10-312-841-2	Sequence 2, Appli
1227	38.6	1.7	284	18	US-10-425-115-23704	Sequence 23704, A
c1228	38.6	1.7	1091	17	US-10-424-599-24484	Sequence 24484, A
1229	38.6	1.7	1251	18	US-10-437-963-40466	Sequence 40466, A

1230	38.6	1.7	1466	18	US-10-437-963-92376	Sequence 92376, A
1231	38.6	1.7	1494	17	US-10-359-369-3	Sequence 3, Appli
1232	38.6	1.7	1759	17	US-10-425-114-28506	Sequence 28506, A
1233	38.6	1.7	1789	18	US-10-425-115-48503	Sequence 48503, A
1234	38.4	1.7	1431	18	US-10-437-963-96756	Sequence 96756, A
1235	38.4	1.7	1524	18	US-10-437-963-23261	Sequence 23261, A
1236	38.4	1.7	1619	18	US-10-425-115-153675	Sequence 153675, A
1237	38.4	1.7	1637	18	US-10-425-115-78687	Sequence 78687, A
1238	38.4	1.7	1638	17	US-10-425-114-35181	Sequence 35181, A
1239	38.4	1.7	1662	17	US-10-424-599-122713	Sequence 122713, A
1240	38.4	1.7	1886	17	US-10-425-114-30306	Sequence 30306, A
1241	38.4	1.7	1999	18	US-10-425-115-78665	Sequence 78665, A
1242	38.4	1.7	6076	15	US-10-240-453-222	Sequence 222, App
1243	38.2	1.6	330	15	US-10-174-693-168	Sequence 168, App
1244	38.2	1.6	1461	18	US-10-437-963-79546	Sequence 79546, A
1245	38.2	1.6	1807	17	US-10-425-114-15670	Sequence 15670, A
1246	38.2	1.6	1937	18	US-10-425-115-39145	Sequence 39145, A
c1247	38.2	1.6	25138	18	US-10-832-777-18	Sequence 18, Appl
c1248	38.2	1.6	25138	19	US-10-832-622B-18	Sequence 18, Appl
1249	38	1.6	1341	18	US-10-437-963-92129	Sequence 92129, A
1250	38	1.6	1704	18	US-10-437-963-16477	Sequence 16477, A
1251	38	1.6	1726	17	US-10-425-114-20709	Sequence 20709, A
1252	38	1.6	1761	17	US-10-425-114-28838	Sequence 28838, A
1253	38	1.6	1830	18	US-10-425-115-153419	Sequence 153419, A
1254	38	1.6	2089	18	US-10-425-115-82093	Sequence 82093, A
c1255	37.8	1.6	588	13	US-10-027-632-240503	Sequence 240503, A
c1256	37.8	1.6	588	17	US-10-027-632-240503	Sequence 240503, A
1257	37.8	1.6	1470	17	US-10-425-114-27785	Sequence 27785, A
1258	37.8	1.6	7001	15	US-10-172-086-59	Sequence 59, Appl
1259	37.8	1.6	7001	18	US-10-311-507-1	Sequence 1, Appli
1260	37.8	1.6	7001	18	US-10-480-846-59	Sequence 59, Appl
1261	37.6	1.6	121	10	US-09-818-875-4012	Sequence 4012, Ap
c1262	37.6	1.6	121	10	US-09-818-875-4013	Sequence 4013, Ap
1263	37.6	1.6	121	17	US-10-209-787-4012	Sequence 4012, Ap
c1264	37.6	1.6	121	17	US-10-209-787-4013	Sequence 4013, Ap
1265	37.6	1.6	121	17	US-10-261-185-4012	Sequence 4012, Ap
c1266	37.6	1.6	121	17	US-10-261-185-4013	Sequence 4013, Ap
1267	37.6	1.6	121	18	US-10-681-074-4012	Sequence 4012, Ap
c1268	37.6	1.6	121	18	US-10-681-074-4013	Sequence 4013, Ap
c1269	37.6	1.6	482	15	US-10-002-623-648	Sequence 648, App
c1270	37.6	1.6	577	18	US-10-437-963-97351	Sequence 97351, A
c1271	37.6	1.6	689	18	US-10-437-963-88613	Sequence 88613, A
1272	37.6	1.6	823	18	US-10-767-701-1703	Sequence 1703, Ap
1273	37.6	1.6	902	17	US-10-424-599-4612	Sequence 4612, Ap
1274	37.6	1.6	1286	17	US-10-425-114-6750	Sequence 6750, Ap
1275	37.6	1.6	1299	17	US-10-424-599-65544	Sequence 65544, A
1276	37.6	1.6	1461	18	US-10-437-963-42611	Sequence 42611, A
1277	37.6	1.6	1510	18	US-10-425-115-38054	Sequence 38054, A
c1278	37.6	1.6	1575	17	US-10-282-122A-19422	Sequence 19422, A
1279	37.6	1.6	1637	17	US-10-425-114-28278	Sequence 28278, A
1280	37.6	1.6	1907	17	US-10-424-599-128627	Sequence 128627, A
1281	37.6	1.6	1980	18	US-10-425-115-38076	Sequence 38076, A
1282	37.6	1.6	6191	15	US-10-311-455-1190	Sequence 1190, Ap
1283	37.6	1.6	8771	15	US-10-311-455-1798	Sequence 1798, Ap
1284	37.6	1.6	54169	13	US-10-087-192-1486	Sequence 1486, Ap
c1285	37.4	1.6	526	16	US-10-029-386-10009	Sequence 10009, A
c1286	37.4	1.6	719	17	US-10-424-599-97308	Sequence 97308, A

1287	37.4	1.6	882	17	US-10-282-122A-10822	Sequence 10822, A
c1288	37.4	1.6	1364	18	US-10-437-963-31084	Sequence 31084, A
1289	37.4	1.6	1365	16	US-10-167-547C-19	Sequence 19, Appl
1290	37.4	1.6	1368	9	US-09-938-842A-1384	Sequence 1384, Ap
1291	37.4	1.6	1368	11	US-09-938-842A-1384	Sequence 1384, Ap
1292	37.4	1.6	1404	9	US-09-938-842A-2210	Sequence 2210, Ap
1293	37.4	1.6	1404	11	US-09-938-842A-2210	Sequence 2210, Ap
1294	37.4	1.6	1404	17	US-10-203-319A-37	Sequence 37, Appl
1295	37.4	1.6	1458	17	US-10-424-599-40439	Sequence 40439, A
1296	37.4	1.6	1675	18	US-10-739-930-267	Sequence 267, App
c1297	37.4	1.6	1677	18	US-10-437-963-97384	Sequence 97384, A
1298	37.4	1.6	1777	17	US-10-425-114-27455	Sequence 27455, A
c1299	37.4	1.6	2127	17	US-10-282-122A-36054	Sequence 36054, A
1300	37.4	1.6	2503	18	US-10-425-115-177938	Sequence 177938,
1301	37.2	1.6	1089	17	US-10-424-599-93217	Sequence 93217, A
1302	37.2	1.6	1110	15	US-10-259-165-305	Sequence 305, App
1303	37.2	1.6	3502	17	US-10-282-122A-35837	Sequence 35837, A
1304	37.2	1.6	3524	17	US-10-108-260A-454	Sequence 454, App
c1305	37.2	1.6	54169	13	US-10-087-192-1486	Sequence 1486, Ap
1306	37.2	1.6	161280	15	US-10-144-649A-746	Sequence 746, App
c1307	37	1.6	537	9	US-09-770-152-739	Sequence 739, App
1308	37	1.6	572	13	US-10-027-632-233057	Sequence 233057,
1309	37	1.6	572	17	US-10-027-632-233057	Sequence 233057,
c1310	37	1.6	602	13	US-10-027-632-93890	Sequence 93890, A
c1311	37	1.6	602	13	US-10-027-632-93891	Sequence 93891, A
c1312	37	1.6	602	17	US-10-027-632-93890	Sequence 93890, A
c1313	37	1.6	602	17	US-10-027-632-93891	Sequence 93891, A
1314	37	1.6	779	18	US-10-425-115-13372	Sequence 13372, A
c1315	37	1.6	876	18	US-10-425-115-144071	Sequence 144071,
c1316	37	1.6	1170	10	US-09-813-432-45	Sequence 45, Appl
c1317	37	1.6	1170	10	US-09-813-432-46	Sequence 46, Appl
c1318	37	1.6	1170	17	US-10-174-364-45	Sequence 45, Appl
c1319	37	1.6	1170	17	US-10-174-364-46	Sequence 46, Appl
c1320	37	1.6	1170	17	US-10-246-583-45	Sequence 45, Appl
c1321	37	1.6	1170	17	US-10-246-583-46	Sequence 46, Appl
c1322	37	1.6	1170	18	US-10-689-832-45	Sequence 45, Appl
c1323	37	1.6	1170	18	US-10-689-832-46	Sequence 46, Appl
1324	37	1.6	1260	18	US-10-437-963-24189	Sequence 24189, A
1325	37	1.6	1365	16	US-10-167-547C-17	Sequence 17, Appl
1326	37	1.6	1401	18	US-10-437-963-24188	Sequence 24188, A
1327	37	1.6	1446	9	US-09-938-842A-1812	Sequence 1812, Ap
1328	37	1.6	1446	11	US-09-938-842A-1812	Sequence 1812, Ap
1329	37	1.6	1452	18	US-10-437-963-7986	Sequence 7986, Ap
1330	37	1.6	1770	17	US-10-425-114-25086	Sequence 25086, A
1331	37	1.6	1770	18	US-10-425-115-165209	Sequence 165209,
1332	37	1.6	1819	17	US-10-425-114-10640	Sequence 10640, A
1333	37	1.6	1836	17	US-10-424-599-49479	Sequence 49479, A
1334	37	1.6	1967	18	US-10-437-963-75197	Sequence 75197, A
c1335	37	1.6	2145	10	US-09-813-432-13	Sequence 13, Appl
c1336	37	1.6	2145	17	US-10-174-364-13	Sequence 13, Appl
c1337	37	1.6	2145	17	US-10-246-583-13	Sequence 13, Appl
c1338	37	1.6	2145	18	US-10-689-832-13	Sequence 13, Appl
c1339	37	1.6	2600	18	US-10-343-903-43	Sequence 43, Appl
c1340	37	1.6	3435	9	US-09-803-670-1	Sequence 1, Appli
1341	37	1.6	5666	15	US-10-311-455-1745	Sequence 1745, Ap
c1342	37	1.6	8064	15	US-10-311-455-1359	Sequence 1359, Ap
c1343	37	1.6	8868	9	US-09-803-670-3	Sequence 3, Appli

1344	37	1.6	23934	9	US-09-764-860-777	Sequence 777, App
c1345	37	1.6	23934	9	US-09-764-877-2536	Sequence 2536, Ap
1346	37	1.6	23934	9	US-09-764-877-2544	Sequence 2544, Ap
c1347	37	1.6	23934	10	US-09-764-891-7210	Sequence 7210, Ap
1348	37	1.6	23934	14	US-10-074-095-777	Sequence 777, App
1349	37	1.6	23934	17	US-10-212-872-777	Sequence 777, App
c1350	37	1.6	23934	17	US-10-242-515-2536	Sequence 2536, Ap
1351	37	1.6	23934	17	US-10-242-515-2544	Sequence 2544, Ap
1352	37	1.6	145806	18	US-10-719-993-6943	Sequence 6943, Ap
1353	37	1.6	684187	18	US-10-367-094-71	Sequence 71, Appl
1354	36.8	1.6	550	18	US-10-357-930-57145	Sequence 57145, A
1355	36.8	1.6	590	18	US-10-425-115-124593	Sequence 124593,
1356	36.8	1.6	624	18	US-10-767-701-3164	Sequence 3164, Ap
1357	36.8	1.6	682	13	US-10-027-632-218368	Sequence 218368,
1358	36.8	1.6	682	17	US-10-027-632-218368	Sequence 218368,
1359	36.8	1.6	697	17	US-10-424-599-52324	Sequence 52324, A
1360	36.8	1.6	746	14	US-10-205-522-2	Sequence 2, Appli
1361	36.8	1.6	936	18	US-10-473-144-4	Sequence 4, Appli
1362	36.8	1.6	1001	17	US-10-294-934-381	Sequence 381, App
1363	36.8	1.6	1001	17	US-10-294-934-382	Sequence 382, App
1364	36.8	1.6	1041	9	US-09-916-790-3	Sequence 3, Appli
1365	36.8	1.6	1041	17	US-10-678-786-3	Sequence 3, Appli
1366	36.8	1.6	1272	18	US-10-473-144-1	Sequence 1, Appli
1367	36.8	1.6	1275	9	US-09-734-032-1	Sequence 1, Appli
1368	36.8	1.6	1275	13	US-10-016-985-1	Sequence 1, Appli
1369	36.8	1.6	1275	18	US-10-473-144-7	Sequence 7, Appli
1370	36.8	1.6	1282	18	US-10-322-281-37	Sequence 37, Appl
1371	36.8	1.6	1441	10	US-09-890-688-159	Sequence 159, App
1372	36.8	1.6	1473	13	US-10-016-985-3	Sequence 3, Appli
1373	36.8	1.6	1650	17	US-10-282-122A-25691	Sequence 25691, A
1374	36.8	1.6	1829	9	US-09-731-872-238	Sequence 238, App
1375	36.8	1.6	1829	10	US-09-876-997-238	Sequence 238, App
1376	36.8	1.6	1874	15	US-10-180-375-127	Sequence 127, App
1377	36.8	1.6	1874	17	US-10-183-687-143	Sequence 143, App
1378	36.8	1.6	1982	18	US-10-473-144-9	Sequence 9, Appli
1379	36.8	1.6	2060	17	US-10-288-798-25	Sequence 25, Appl
1380	36.8	1.6	2060	17	US-10-362-892-25	Sequence 25, Appl
1381	36.8	1.6	2196	17	US-10-282-122A-25382	Sequence 25382, A
1382	36.8	1.6	2598	9	US-09-816-094-1	Sequence 1, Appli
1383	36.8	1.6	2598	14	US-10-233-613-1	Sequence 1, Appli
1384	36.8	1.6	2598	17	US-10-639-429-1	Sequence 1, Appli
1385	36.8	1.6	2893	9	US-09-916-790-1	Sequence 1, Appli
1386	36.8	1.6	2893	17	US-10-678-786-1	Sequence 1, Appli
1387	36.8	1.6	5464	17	US-10-240-454-38	Sequence 38, Appl
1388	36.8	1.6	9997	15	US-10-311-455-342	Sequence 342, App
1389	36.8	1.6	9997	15	US-10-240-485-38	Sequence 38, Appl
1390	36.8	1.6	10254	15	US-10-311-455-1048	Sequence 1048, Ap
1391	36.8	1.6	12393	15	US-10-311-455-1235	Sequence 1235, Ap
1392	36.8	1.6	17421	14	US-10-239-676-54	Sequence 54, Appl
1393	36.8	1.6	17421	15	US-10-240-453-56	Sequence 56, Appl
1394	36.8	1.6	34688	18	US-10-433-793-89	Sequence 89, Appl
1395	36.8	1.6	73334	15	US-10-311-455-2098	Sequence 2098, Ap
1396	36.8	1.6	73334	17	US-10-240-589C-128	Sequence 128, App
1397	36.6	1.6	324	18	US-10-437-963-91462	Sequence 91462, A
1398	36.6	1.6	363	18	US-10-437-963-44337	Sequence 44337, A
1399	36.6	1.6	667	18	US-10-767-701-3793	Sequence 3793, Ap
1400	36.6	1.6	1260	17	US-10-282-122A-38427	Sequence 38427, A

1401	36.6	1.6	1747	18	US-10-739-930-3952	Sequence 3952, Ap
1402	36.6	1.6	1830	16	US-10-247-671-54	Sequence 54, Appl
1403	36.6	1.6	1980	17	US-10-425-114-24536	Sequence 24536, A
1404	36.6	1.6	2023	18	US-10-425-115-93285	Sequence 93285, A
1405	36.6	1.6	3401	18	US-10-755-889-493	Sequence 493, App
1406	36.6	1.6	3401	18	US-10-370-715B-153	Sequence 153, App
1407	36.6	1.6	4040	13	US-10-044-090-656	Sequence 656, App
1408	36.6	1.6	19806	13	US-10-118-037-3	Sequence 3, Appli
1409	36.6	1.6	19806	19	US-10-924-785-3	Sequence 3, Appli
1410	36.6	1.6	37180	18	US-10-367-094-13	Sequence 13, Appl
c1411	36.6	1.6	684187	18	US-10-367-094-71	Sequence 71, Appl
c1412	36.6	1.6	3673778	16	US-10-312-841-1	Sequence 1, Appli
1413	36.4	1.6	585	17	US-10-260-238-4093	Sequence 4093, Ap
1414	36.4	1.6	676	13	US-10-027-632-206893	Sequence 206893,
1415	36.4	1.6	676	17	US-10-027-632-206893	Sequence 206893,
1416	36.4	1.6	705	13	US-10-027-632-13862	Sequence 13862, A
1417	36.4	1.6	705	17	US-10-027-632-13862	Sequence 13862, A
1418	36.4	1.6	706	18	US-10-767-701-5342	Sequence 5342, Ap
1419	36.4	1.6	718	17	US-10-260-238-4094	Sequence 4094, Ap
1420	36.4	1.6	761	17	US-10-260-238-2807	Sequence 2807, Ap
1421	36.4	1.6	864	17	US-10-260-238-2799	Sequence 2799, Ap
c1422	36.4	1.6	1044	17	US-10-424-599-103983	Sequence 103983,
1423	36.4	1.6	1077	18	US-10-828-924-65	Sequence 65, Appl
1424	36.4	1.6	1266	17	US-10-138-588-31	Sequence 31, Appl
1425	36.4	1.6	1266	17	US-10-210-172-173	Sequence 173, App
1426	36.4	1.6	1278	18	US-10-804-677-3	Sequence 3, Appli
1427	36.4	1.6	1952	17	US-10-424-599-33433	Sequence 33433, A
c1428	36.4	1.6	2277	18	US-10-437-963-57533	Sequence 57533, A
c1429	36.4	1.6	6620	14	US-10-239-676-196	Sequence 196, App
c1430	36.4	1.6	6620	15	US-10-240-453-290	Sequence 290, App
1431	36.4	1.6	8675	18	US-10-804-677-18	Sequence 18, Appl
1432	36.4	1.6	10957	15	US-10-311-455-1083	Sequence 1083, Ap
c1433	36.4	1.6	19734	15	US-10-311-455-1906	Sequence 1906, Ap
1434	36.4	1.6	153995	18	US-10-322-281-721	Sequence 721, App
c1435	36.4	1.6	158091	17	US-10-235-192A-38	Sequence 38, Appl
1436	36.4	1.6	321019	19	US-10-741-600-17566	Sequence 17566, A
1437	36.4	1.6	329019	18	US-10-388-838-48	Sequence 48, Appl
1438	36.4	1.6	1790242	18	US-10-719-993-6940	Sequence 6940, Ap
1439	36.2	1.6	342	18	US-10-425-115-2548	Sequence 2548, Ap
c1440	36.2	1.6	594	14	US-10-123-155-10	Sequence 10, Appl
c1453	36.2	1.6	667	9	US-09-770-149-435	Sequence 435, App
1454	36.2	1.6	1512	18	US-10-437-963-51054	Sequence 51054, A
1455	36.2	1.6	1853	17	US-10-424-599-62199	Sequence 62199, A
c1456	36.2	1.6	2093	18	US-10-739-930-3199	Sequence 3199, Ap
1457	36.2	1.6	2988	9	US-09-815-242-4196	Sequence 4196, Ap
1458	36.2	1.6	3030	9	US-09-815-242-8043	Sequence 8043, Ap
c1459	36.2	1.6	3129	9	US-09-739-254-18	Sequence 18, Appl
c1460	36.2	1.6	3129	9	US-09-904-615-18	Sequence 18, Appl
c1461	36.2	1.6	3129	14	US-10-054-988-18	Sequence 18, Appl
1462	36.2	1.6	11122	11	US-09-984-429-394	Sequence 394, App
1463	36.2	1.6	11122	11	US-09-984-429-444	Sequence 444, App
1464	36.2	1.6	11172	9	US-09-764-878-231	Sequence 231, App
1465	36.2	1.6	11172	14	US-10-079-854-231	Sequence 231, App
1466	36.2	1.6	12507	15	US-10-311-455-272	Sequence 272, App
1467	36.2	1.6	33053	18	US-10-433-793-36	Sequence 36, Appl
1468	36.2	1.6	59110	19	US-10-741-600-17742	Sequence 17742, A
c1469	36.2	1.6	98829	14	US-10-017-724-3	Sequence 3, Appli

1470	36.2	1.6	101507	18	US-10-719-993-6772	Sequence 6772, Ap
c1471	36.2	1.6	126001	17	US-10-175-492-13	Sequence 13, Appl
1472	36	1.6	279	9	US-09-923-876-4101	Sequence 4101, Ap
1473	36	1.6	279	10	US-09-923-876-4101	Sequence 4101, Ap
1474	36	1.6	527	16	US-10-029-386-8998	Sequence 8998, Ap
1475	36	1.6	719	17	US-10-431-252-16	Sequence 16, Appl
1476	36	1.6	928	18	US-10-425-115-118323	Sequence 118323,
1477	36	1.6	936	18	US-10-437-963-82677	Sequence 82677, A
c1478	36	1.6	1069	13	US-10-027-632-117075	Sequence 117075,
c1479	36	1.6	1069	17	US-10-027-632-117075	Sequence 117075,
1480	36	1.6	1170	17	US-10-282-122A-26573	Sequence 26573, A
1481	36	1.6	1188	18	US-10-437-963-48852	Sequence 48852, A
1482	36	1.6	1227	17	US-10-282-122A-28218	Sequence 28218, A
1483	36	1.6	1314	17	US-10-431-252-6	Sequence 6, Appli
1484	36	1.6	1377	18	US-10-437-963-2013	Sequence 2013, Ap
1485	36	1.6	1496	17	US-10-425-114-29436	Sequence 29436, A
1486	36	1.6	1536	17	US-10-282-122A-18370	Sequence 18370, A
1487	36	1.6	1574	17	US-10-431-252-15	Sequence 15, Appl
1488	36	1.6	1681	18	US-10-425-115-52517	Sequence 52517, A
1489	36	1.6	1866	18	US-10-437-963-91652	Sequence 91652, A
1490	36	1.6	1928	17	US-10-424-599-129209	Sequence 129209,
1491	36	1.6	2165	17	US-10-431-252-14	Sequence 14, Appl
1492	36	1.6	2336	17	US-10-431-252-2	Sequence 2, Appli
1493	36	1.6	2391	17	US-10-424-599-4593	Sequence 4593, Ap
1494	36	1.6	3684	17	US-10-431-252-19	Sequence 19, Appl
1495	36	1.6	3939	17	US-10-431-252-22	Sequence 22, Appl
1496	36	1.6	3963	17	US-10-431-252-20	Sequence 20, Appl
1497	36	1.6	3979	18	US-10-776-311-90	Sequence 90, Appl
1498	36	1.6	3985	17	US-10-431-252-18	Sequence 18, Appl
1499	36	1.6	4550	13	US-10-117-846-9	Sequence 9, Appli
1500	36	1.6	4827	17	US-10-431-252-21	Sequence 21, Appl

Search completed: February 15, 2005, 07:50:07

Job time : 4639 secs